GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 22, 2005, 07:16:57 ; Search time 5792.24 Seconds
(without alignments)
11720.367 Million cell updates/sec

Title: US-10-054-680-3
Perfect score: 1863
Sequence: 1 atggcgtggttaaggttgca.....ggaaagccagtattgggtga 1863

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1784.4	95.8	1788	9	AY401283	AY401283 Homo sapi
2	1783	95.7	3186	3	BC036783	BC036783 Homo sapi
3	1739.4	93.4	1788	9	AY401284	AY401284 Pan trogl
4	1544.4	82.9	1788	9	AY401285	AY401285 Mus muscu
5	1521	81.6	2534	3	AK044636	AK044636 Mus muscu
6	971	52.1	1589	3	CNSLT1IBJ	BX248763 human ful
7	899.2	48.3	938	5	BX374548	BX374548 BX374548
8	805	43.2	887	4	BI913344	BI913344 603178823

	9	784.8	42.1	2922	9	AY398961	AY398961 Homo sapi
	10	768.2	41.2	939	5	BX347210	BX347210 BX347210
	11	755	40.5	2922	9	AY398963	AY398963 Mus muscu
	12	739.8	39.7	792	4	BI522813	BI522813 603175911
	13	737.8	39.6	916	5	BX368185	BX368185 BX368185
	14	710.4	38.1	4374	3	AK035163	AK035163 Mus muscu
	15	708.4	38.0	894	5	BX390204	BX390204 BX390204
	16	673.2	36.1	775	5	BQ770745	BQ770745 UI-M-FI0-
	17	638	34.2	3573	3	AK048160	AK048160 Mus muscu
	18	635.4	34.1	2516	9	AY408693	AY408693 Homo sapi
	19	607	32.6	2881	9	AY398962	AY398962 Pan trogl
	20	598.6	32.1	944	5	BX368184	BX368184 BX368184
c	21	579.2	31.1	753	9	AG462634	AG462634 Mus muscu
	22	574.6	30.8	752	7	CF532853	CF532853 UI-M-GH0-
c	23	553.6	29.7	1062	9	CNS04DXR	AL286344 Tetraodon
	24	503.8	27.0	588	7	CF533347	CF533347 UI-M-FY0-
	25	497	26.7	704	7	CF729293	CF729293 UI-M-HD0-
	26	483.2	25.9	851	5	BX325851	BX325851 BX325851
	27	456.8	24.5	676	2	BB280958	BB280958 BB280958
	28	412.4	22.1	503	8	BZ211245	BZ211245 CH230-426
c	29	407.4	21.9	499	8	BH349372	BH349372 CH230-32M
	30	403.4	21.7	2515	9	AY408695	AY408695 Mus muscu
	31	397.2	21.3	911	5	BU901346	BU901346 AGENCOURT
	32	368.4	19.8	1139	5	BX355386	BX355386 BX355386
	33	363.6	19.5	829	9	CC501501	CC501501 CH240_339
	34	359	19.3	569	4	BI906774	BI906774 603064517
	35	352	18.9	741	7	CF539360	CF539360 UI-M-GH0-
	36	341.2	18.3	830	5	BU747974	BU747974 CH3#016_H
c	37	339.4	18.2	833	5	BU747973	BU747973 CH3#016_H
c	38	338	18.1	1020	9	CNS03Y28	AL265769 Tetraodon
	39	327.4	17.6	2472	9	AY408694	AY408694 Pan trogl
c	40	320	17.2	384	8	AZ258968	AZ258968 RPCI-23-1
c	41	304.4	16.3	818	8	BZ163286	BZ163286 CH230-276
	42	303	16.3	462	1	AL712986	AL712986 DKFZp686J
	43	298.4	16.0	767	7	CR426134	CR426134 CR426134
	44	295.8	15.9	693	2	BB648018	BB648018 BB648018
c	45	294.2	15.8	551	9	FR0052027	AL688306 Fugu rubr

ALIGNMENTS

RESULT 1
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LOCUS AY401283 1788 bp DNA linear GSS 15-DEC-2003
DEFINITION Homo sapiens SLC8A3 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY401283
VERSION AY401283.1 GI:39757272
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1788)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,

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            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 1788)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            <1. .>1788
                     /gene="SLC8A3"
                     /locus_tag="HCM0839"
ORIGIN

  Query Match             95.8%;  Score 1784.4;  DB 9;  Length 1788;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1785;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Db        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Db        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Db        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Db        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Db        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Db        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Db       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Db       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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RESULT 2
BC036783
LOCUS       BC036783                3186 bp    mRNA    linear   HTC 19-NOV-2003
DEFINITION  Homo sapiens solute carrier family 8 (sodium-calcium exchanger),
            member 3, mRNA (cDNA clone IMAGE:5732743), with apparent retained
            intron.
ACCESSION   BC036783
VERSION     BC036783.1  GI:23331089
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3186)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
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Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

REFERENCE 2 (bases 1 to 3186)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (23-AUG-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov

COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Invitrogen
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 79 Row: j Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 17865803
This clone has the following problem: retained intron.

FEATURES Location/Qualifiers

source 1. .3186
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5732743"
/tissue_type="Brain, hippocampus"

/clone_lib="NIH_MGC_124"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 95.7%; Score 1783; DB 3; Length 3186;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1812; Conservative 0; Mismatches 25; Indels 4; Gaps 1;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Db        678 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 737

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db        738 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAG 797

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db        798 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 857

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db       1098 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 1157

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db       1158 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1217

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Db       1218 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1277
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Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db       1278 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1337

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1338 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 1397

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Db       1398 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 1457

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Db       1458 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1517

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Db       1518 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1577

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Db       1578 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1637

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Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Db       1878 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1937

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Db       1998 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 2057

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Db       2058 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 2117

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Db       2178 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 2237

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db       2238 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2297

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
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Db       2298 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 2353

Qy       1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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Db       2354 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 2394
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RESULT 3
AY401284

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LOCUS       AY401284                1788 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Pan troglodytes SLC8A3 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY401284
VERSION     AY401284.1  GI:39757273
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 1788)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 1788)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .1788
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                     /mol_type="genomic DNA"
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/locus_tag="HCM0839"

ORIGIN

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Best Local Similarity 97.8%; Pred. No. 0;
Matches 1746; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTGTGCTCTTTCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCG 300

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Db        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACGATTAAGAAACCCAATGGAGAA 360

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Db        361 ACCAGCACAACCACTATTCGAGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCACCTA 600

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Db        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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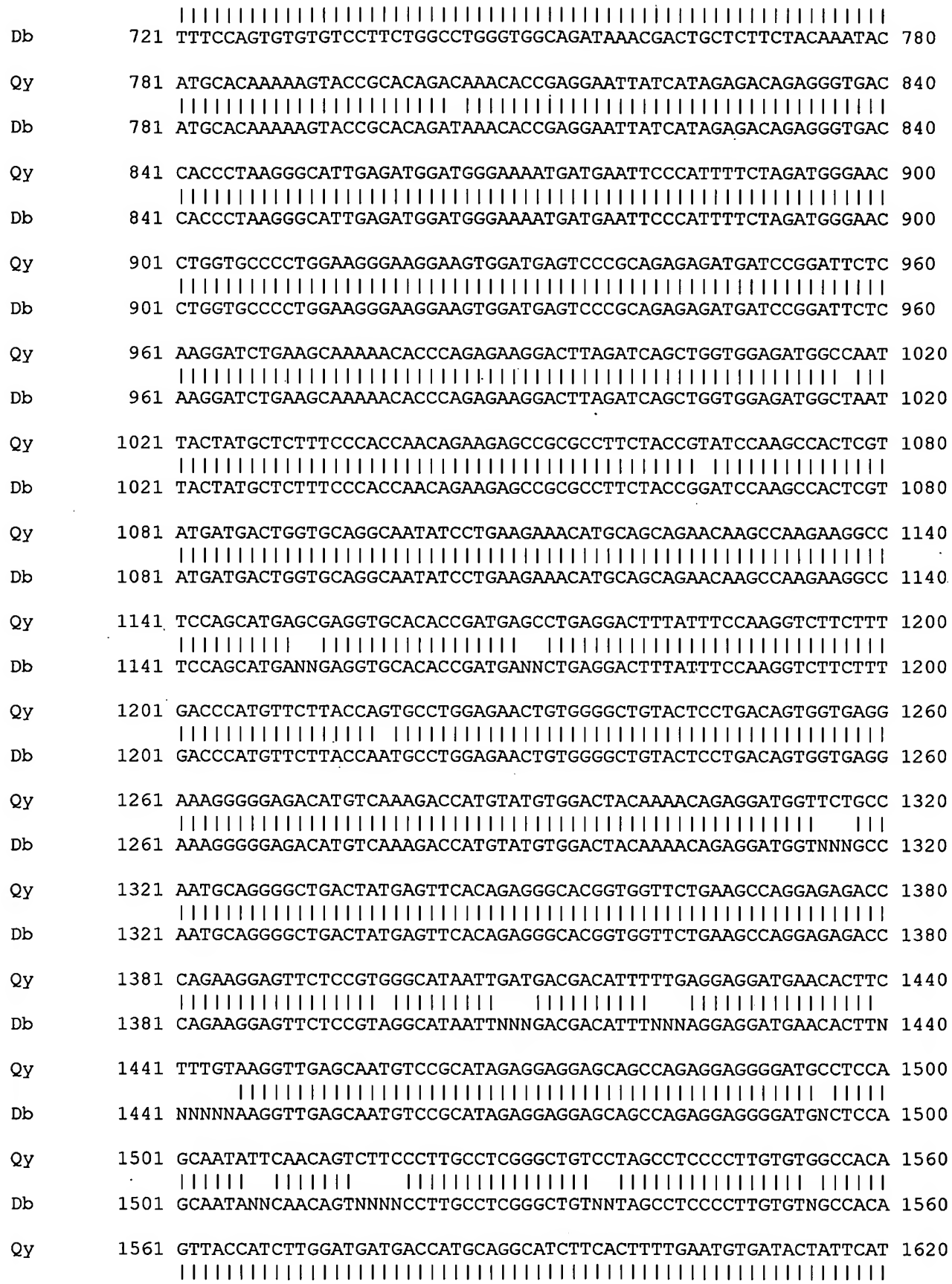

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Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Db       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
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Db       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGT 1786
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RESULT 4
AY401285

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LOCUS       AY401285                1788 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Mus musculus SLC8A3 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY401285
VERSION     AY401285.1  GI:39757274
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1788)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 1788)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .1788
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     gene            <1. .>1788
                     /gene="SLC8A3"
                     /locus_tag="HCM0839"
ORIGIN
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Query Match 82.9%; Score 1544.4; DB 9; Length 1788;

Best Local Similarity 91.5%; Pred. No. 0;
Matches 1635; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db          1 ATGGCGTGGTTACGGCTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACT 60

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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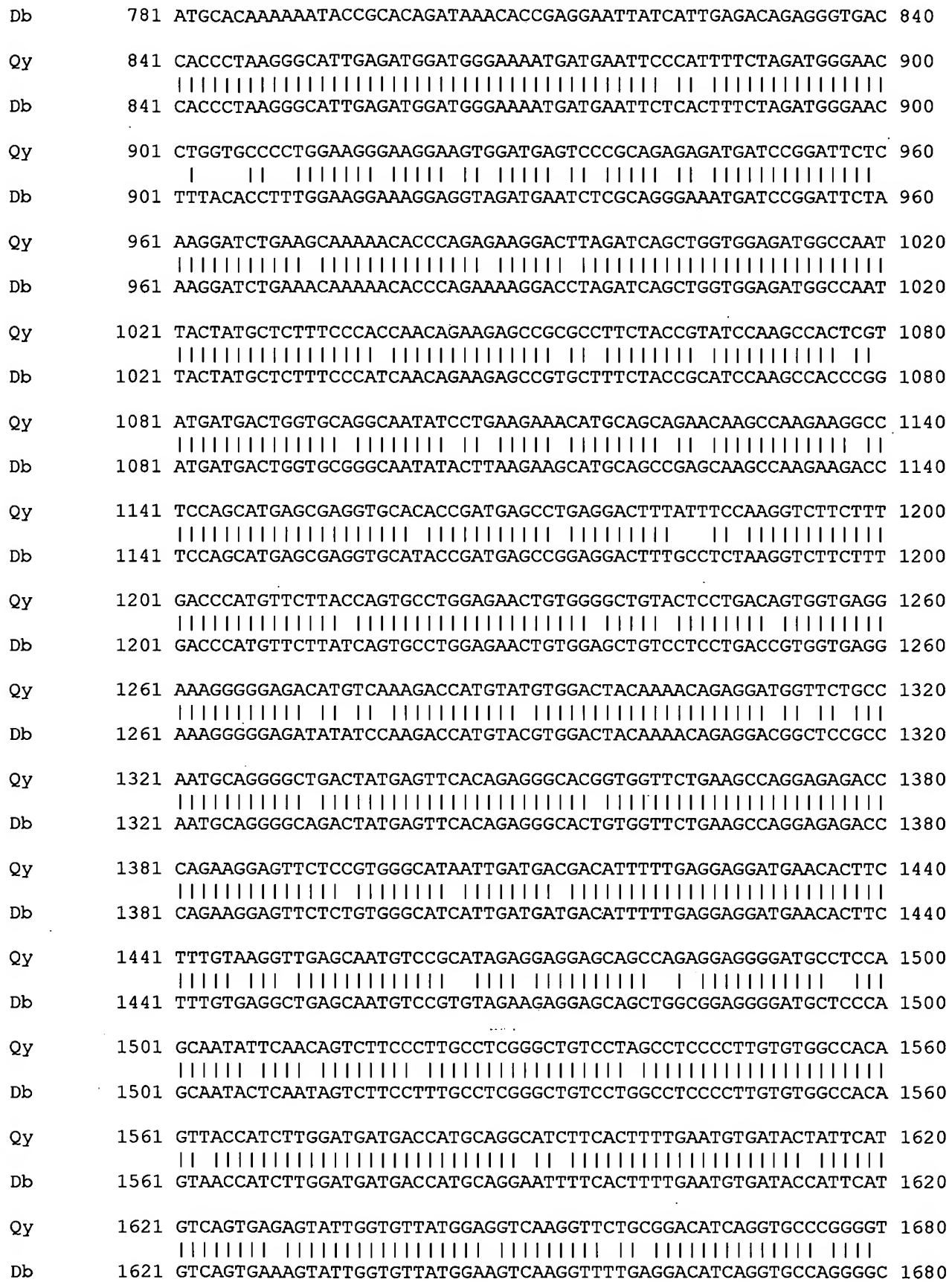

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Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
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Db       1741 GAAGATGCATATGGGGAGCTGGAGTTCAAGAATGATGAAACAGTGT 1786
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RESULT 5
AK044636

LOCUS AK044636 2534 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus adult retina cDNA, RIKEN full-length enriched library, clone:A930029A02 product:solute carrier family 8 (sodium/calcium exchanger), member 3, full insert sequence.
ACCESSION AK044636
VERSION AK044636.1 GI:26336660
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 2534)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Retina RNA was provided by Dr. Stefano Gustincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA) whose assistance is gratefully acknowledged. Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
FEATURES Location/Qualifiers
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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ORIGIN

Query Match 81.6%; Score 1521; DB 3; Length 2534;
Best Local Similarity 90.2%; Pred. No. 0;
Matches 1662; Conservative 0; Mismatches 175; Indels 6; Gaps 3;

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Db        603 ATGGCGTGGTTACGGCTGCACCCTCTCACCTCTGCCTTCCTCCATCTTGGGCCTGGTTAC 662

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Db        663 TTTTGTGCTCTTCCTGAATTGTCTTCGAGCAGAGGCTGGTGACTCGGGGGATGTGCCCAG 722

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Db        723 TGCAGGGCAGAACAATGAGTCCTGTTCGGGGTCATCAGACTGCAAGGAGGGTGTCATTTT 782

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Qy        599 TACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGA 658
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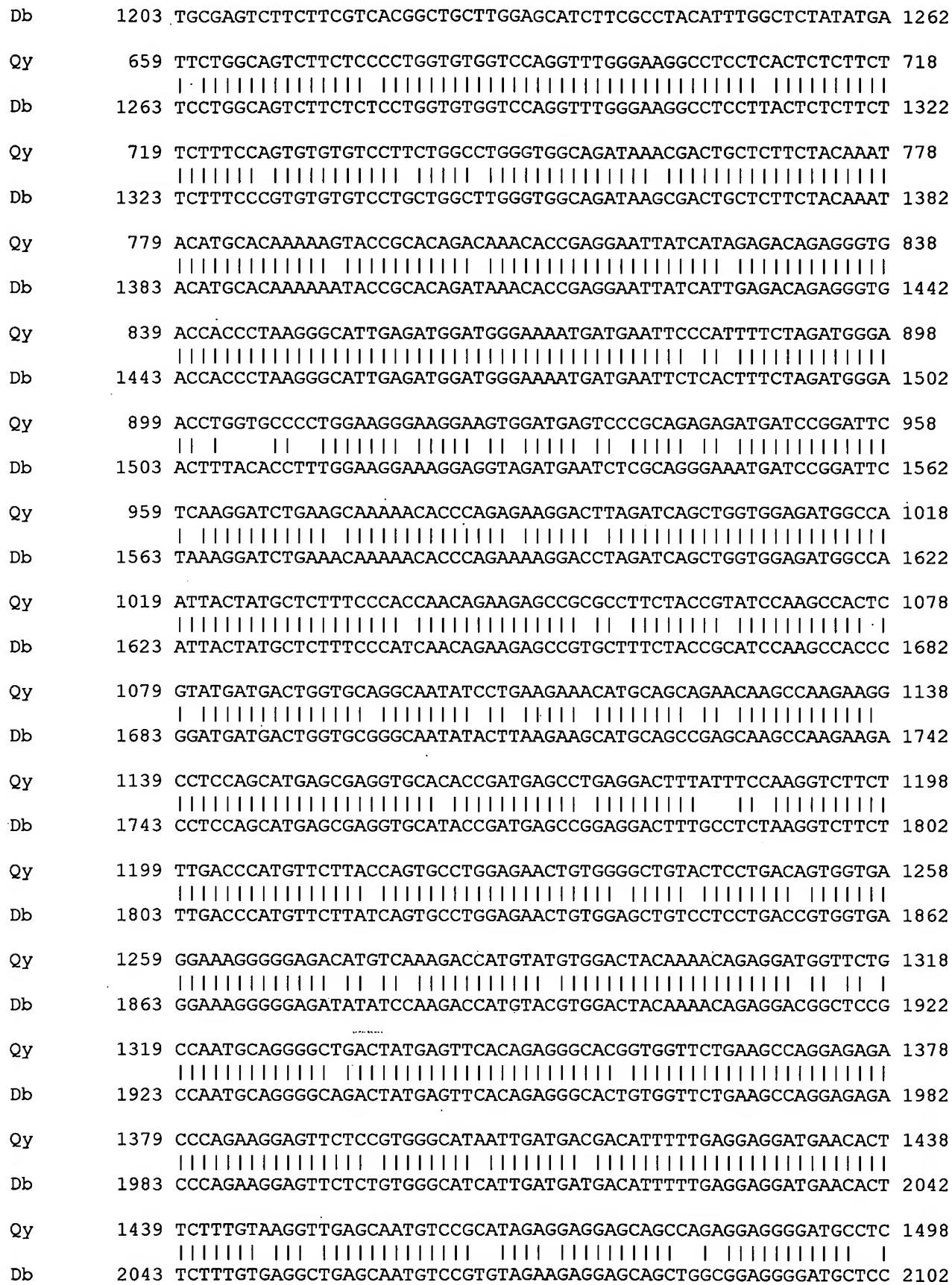

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Qy       1679 GTACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACT 1738
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Qy       1739 TTGAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGG 1798
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RESULT 6
CNSLT1IBJ
LOCUS       CNSLT1IBJ               1589 bp    mRNA    linear   HTC 18-JUN-2003
DEFINITION  human full-length cDNA 5-PRIME end of clone CS0DB006YD18 of
            Neuroblastoma of Homo sapiens (human).
ACCESSION   BX248763
VERSION     BX248763.1  GI:28375580
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1589)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished
  REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue
REFERENCE   2  (bases 1 to 1589)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-2003) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen.
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches  971;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       1579 AAGGATCTGAA 1589
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RESULT 7
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LOCUS       BX374548                938 bp    mRNA    linear   EST 23-APR-2004
DEFINITION  BX374548 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
            cDNA clone CS0DB006YD18 5-PRIME, mRNA sequence.
ACCESSION   BX374548
VERSION     BX374548.2  GI:46558208
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 938)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On May 8, 2003 this sequence version replaced gi:30438490.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
```

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7256.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DB006DB09_DB1287_2&c=7256.r.

FEATURES Location/Qualifiers
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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 48.3%; Score 899.2; DB 5; Length 938;
Best Local Similarity 97.8%; Pred. No. 1.7e-246;
Matches 918; Conservative 0; Mismatches 20; Indels 1; Gaps 1;

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Db          1 CCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCC-GTGTGTGTCCTTCTGGCCTG 59

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Qy       1167 TGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGGA 1226
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Qy       1287 GTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCAC 1346
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Qy       1347 AGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAAT 1406
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Qy       1407 TGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCAT 1466
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Db        780 AGAGGAGGAGCAGCCAGAGGAGGGGATGCCTNNCAGCATATTCAAACAGTCTTCCTTGCC 839

Qy       1527 TCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATGC 1586
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Db        840 TCGGGCTGTCCTAGCCTNCCCTTGNGTGGNCACAGTTACCATCTTGGATGATGACCATGC 899

Qy       1587 AGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAG 1625
               ||||||||||||||||||||||||||||||||||||
Db        900 NAGCATCTTCACTTTTGAATGTGATACTATTCATGTCAG 938
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RESULT 8
BI913344
LOCUS       BI913344                887 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  603178823F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5243308 5',
            mRNA sequence.
ACCESSION   BI913344
VERSION     BI913344.1  GI:16177710
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 887)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
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found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11613 row: m column: 05
High quality sequence stop: 782.

FEATURES Location/Qualifiers
source 1. .887
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5243308"
/lab_host="DH10B"
/clone_lib="NIH_MGC_121"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 43.2%; Score 805; DB 4; Length 887;
Best Local Similarity 98.0%; Pred. No. 2e-219;
Matches 836; Conservative 0; Mismatches 15; Indels 2; Gaps 2;

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Qy        916 GGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAA 975
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAA 60

Qy        976 AAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCC 1035
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCC 120

Qy       1036 CACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCA 1095
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCA 180

Qy       1096 GGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAG 1155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAG 240

Qy       1156 GTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTAC 1215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTAC 300

Qy       1216 CAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATG 1275
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Db        301 CAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATG 360

Qy       1276 TCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGAC 1335
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Db        361 TCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGAC 420

Qy       1336 TATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCC 1395
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Db         421 TATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCC 480

Qy        1396 GTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGC 1455
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Db         481 GTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGC 540

Qy        1456 AATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGT 1515
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Db         541 AATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGT 600

Qy        1516 CTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGAT 1575
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 CTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGAT 660

Qy        1576 GATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATT 1635
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db         661 GATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTA-T 719

Qy        1636 GGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCC 1695
                ||||| ||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db         720 GGTGTAATGGAGGTCAAGGTTCTGCGGACATCATGTGCCCGGGGTACAGTCATCGTCCCC 779

Qy        1696 TTT-AGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGG 1754
                ||| ||||||| |||||||||||||||||| ||   |  | |   |||||||| ||||||
Db         780 TTTCAGGACAGGAGAAGGGACAGCCAAGGCTGCACGCTAAGGACTTGAAGACCCATATGC 839

Qy        1755 GGAGTTGGAATTC 1767
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Db         840 GGAGTTGGAATTC 852
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RESULT 9
AY398961
LOCUS       AY398961               2922 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Homo sapiens SLC8A1 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY398961
VERSION     AY398961.1  GI:39754950
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2922)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 2922)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
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            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .2922
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            <1. .>2922
                     /gene="SLC8A1"
                     /locus_tag="HCM0065"
ORIGIN
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Query Match 42.1%; Score 784.8; DB 9; Length 2922;
Best Local Similarity 68.3%; Pred. No. 2.1e-213;
Matches 1165; Conservative 0; Mismatches 502; Indels 39; Gaps 4;

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Qy        109 GACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAG 168
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Db        112 GAAATGGAAGGAGAAGGAAATGAAACTGGTGAATGTACTGGATCATATTACTGTAAGAAA 171

Qy        169 GGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGG 228
              || ||  ||  |||| || ||| | ||  |  |||||||  |||||||||| ||||| ||
Db        172 GGGGTGATTTTGCCCATTTGGGAACCCCAAGACCCTTCTTTTGGGGACAAAATTGCTAGA 231

Qy        229 GTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGAC 288
              |  | ||| ||||||||||||| || | |||||||| ||||| || || ||||| |||||
Db        232 GCTACTGTGTATTTTGTGGCCATGGTCTACATGTTTCTTGGAGTCTCTATCATAGCTGAT 291

Qy        289 CGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAA 348
              || |||||| | ||||| |||||||||| |||||||| |  ||  | || || ||||||
Db        292 CGGTTCATGTCCTCTATAGAAGTCATCACATCTCAAGAAAAAGAAATAACCATAAAGAAA 351

Qy        349 CCCAATGGAGAAACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTG 408
              |||||||||| |||| ||  || ||| |  || |||||||||||| || || ||||||
Db        352 CCCAATGGAGAGACCACCAAGACAACTGTGAGGATCTGGAATGAAACAGTTTCTAACCTG 411

Qy        409 ACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGT 468
              ||| | |||||||||| || |||||||||||||| ||||| ||  ||||||| ||||||
Db        412 ACCTTGATGGCCCTGGGATCTTCTGCTCCTGAGATTCTCCTTTCAGTAATTGAAGTGTGT 471

Qy        469 GGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTC 528
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Db        472 GGCCATAACTTCACTGCAGGAGACCTCGGTCCTAGCACCATCGTGGGAAGTGCTGCATTC 531

Qy        529 AACATGTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAG 588
              || |||||||||| ||||   ||||||| || ||| | || ||||||||||  | |||
Db        532 AATATGTTCATCATTATTGCACTCTGTGTTTATGTGGTGCCTGACGGAGAGACAAGGAAG 591

Qy        589 ATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGG 648
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Db        592 ATTAAGCATTTGCGTGTCTTCTTTGTGACAGCAGCCTGGAGCATCTTTGCCTACACCTGG 651

Qy        649 CTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTC 708
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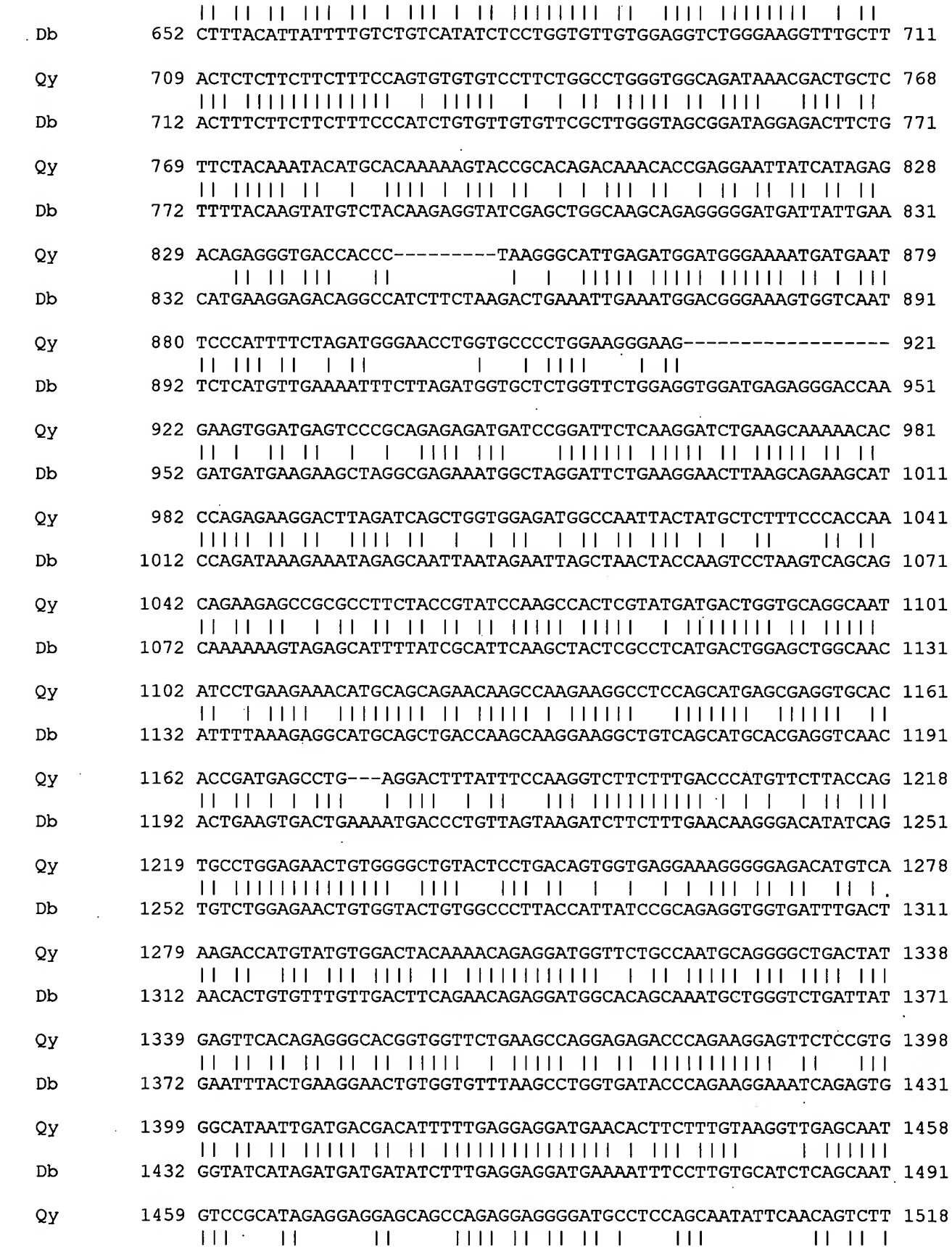

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Db       1492 GTCAAAGTATCTTCTGAAGCTTCAGAAGATGGCATACTGGAAGC---------CAATCAT 1542

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                |   | |  |||  ||| |  || || |     ||||| || || || || ||||||
Db       1543 GTTTCTACACTTGCTTGCCTCGGATCTCCCTCCACTGCCACTGTAACTATTTTTGATGAT 1602

Qy       1579 GACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGT 1638
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Db       1603 GACCACGCAGGCATTTTTACTTTTGAGGAACCTGTGACTCATGTGAGTGAGAGCATTGGC 1662

Qy       1639 GTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCCTTT 1698
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Db       1663 ATCATGGAGGTGAAAGTATTGAGAACATCTGGAGCTCGAGGAAATGTTATCGTTCCATAT 1722

Qy       1699 AGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAG 1758
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Db       1723 AAAACCATCGAAGGGACTGCCAGAGGTGGAGGGGAGGATTTTGAGGACACTTGTGGAGAG 1782

Qy       1759 TTGGAATTCAAGAATGATGAAACTGT 1784
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Db       1783 CTCGAATTCCAGAATGATGAAATTGT 1808
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RESULT 10
BX347210

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LOCUS       BX347210                939 bp    mRNA    linear   EST 23-APR-2004
DEFINITION  BX347210 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
            cDNA clone CS0DB006YD18 5-PRIME, mRNA sequence.
ACCESSION   BX347210
VERSION     BX347210.1  GI:30381158
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 939)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            7256.r
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0BAA004ZB09_CS00355_1&c=7256.r

FEATURES             Location/Qualifiers
     source          1. .939
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
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/clone="CS0DB006YD18"
/tissue_type="NEUROBLASTOMA COT 10-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 41.2%; Score 768.2; DB 5; Length 939;
Best Local Similarity 95.6%; Pred. No. 7.7e-209;
Matches 854; Conservative 0; Mismatches 33; Indels 6; Gaps 6;

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Qy        105 AGGGGACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAA 164
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Db         22 AGGGGACGTGCC-AGCACAGGGCAGAACAATGAGTCCTGTT-AGGGTCATCGGACTGCAA 79

Qy        165 GGAGGGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGC 224
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Db         80 GGAGGGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGC 139

Qy        225 CAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGC 284
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 CAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGC 199

Qy        285 TGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAA 344
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Db        200 TGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAA 259

Qy        345 GAAACCCAATGGAGAAACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAA 404
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Db        260 GAAACCCAATGGAGAAACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAA 319

Qy        405 CCTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGT 464
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Db        320 CCTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGT 379

Qy        465 GTGTGGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGC 524
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 GTGTGGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGC 439

Qy        525 CTTCAACATGTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCG 584
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Db        440 CTTCAACATGTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCG 499

Qy        585 CAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACAT 644
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Db        500 CAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACAT 559

Qy        645 CTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCT 704
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        560 CTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGG-AGGCCT 618

Qy        705 CCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACT 764
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        619 CCTCACTCTCTTCTTC-TTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACT 677
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Qy        765 GCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCAT 824
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Db        678 GCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACAAACACCGAGGGATTTATAT 737

Qy        825 AGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCA 884
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Db        738 AGAGACAGAGGGTGACCACCCTAGGGGCTTTGGGATGGGTGGGAAAAGGATGAATTCCCA 797

Qy        885 TTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGT-CCCGCAGAG 943
              ||||||||  ||||| |  ||||||| |||||||| |||||||| | | |||||||||
Db        798 TTTTCTAGGAGGGAAACCTGTGCCCCCTGAAGGGAAGAAAGTGGATTAATCCCCGCAGAG 857

Qy        944 AGATGATCCGGATTCTC-AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTT 995
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Db        858 AGATGAACCCGGTTCTCTAGGGATCTGAAACCAAAAACCCCCCAAAAAGGCCT 910
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RESULT 11
AY398963
LOCUS       AY398963               2922 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Mus musculus SLC8A1 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY398963
VERSION     AY398963.1  GI:39754952
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2922)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 2922)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .2922
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
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     gene            <1. .>2922
                     /gene="SLC8A1"
                     /locus_tag="HCM0065"
ORIGIN
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Query Match 40.5%; Score 755; DB 9; Length 2922;
Best Local Similarity 67.8%; Pred. No. 7.8e-205;
Matches 1134; Conservative 0; Mismatches 500; Indels 39; Gaps 4;

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Qy      142 TGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTGCCAATCTGGTACCCGGAGAAC 201
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Db      145 TGTACTGGCTCATATTACTGTAAGAAAGGGGTGATCTTGCCCATTTGGGAACCCCAAGAC 204

Qy      202 CCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATG 261
            || ||  |||||||||| ||||| || |  | ||| |||||||||||| || | ||||||
Db      205 CCATCTTTTGGGGACAAAATTGCTAGAGCAACTGTGTATTTTGTGGCCATGGTCTACATG 264

Qy      262 TTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCT 321
            |||||||| || || || ||||| ||||| || ||| | ||||| || ||||||||||||
Db      265 TTCCTTGGAGTTTCTATTATTGCAGACCGGTTTATGTCCTCTATAGAGGTCATCACCTCT 324

Qy      322 CAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAACCACTATTCGG 381
            |||||||  ||  | || || |||||||| |||||||| |||| ||  || ||  |  |
Db      325 CAAGAGAAAGAAATAACGATAAAGAAACCGAATGGAGAGACCACCAAGACGACGGTGAGA 384

Qy      382 GTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAG 441
             ||||||| || ||||| || ||||||||| | |||||||||| || ||||||||||||
Db      385 ATCTGGAACGAGACTGTGTCGAACCTGACCTTGATGGCCCTGGGATCTTCTGCTCCTGAG 444

Qy      442 ATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTCATTGCTGGTGATCTGGGACCT 501
            || ||||| ||  | ||||| ||||| || |||   ||||  || || || ||||| ||
Db      445 ATTCTCCTGTCAGTCATTGAAGTGTGCGGCCATAACTTCACCGCAGGGGACCTGGGTCCC 504

Qy      502 TCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATCATCATTGGCATCTGTGTCTAC 561
               ||||| || || ||||| ||||| |||||||||||||| || |   ||||||| |||
Db      505 AGCACCATCGTGGGAAGTGCTGCCTTTAACATGTTCATCATAATCGCACTCTGTGTTTAC 564

Qy      562 GTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCT 621
            ||| |||| || ||||||||  | |||||||||||||| || || |||||  | || ||
Db      565 GTGGTCCCTGATGGAGAGACAAGGAAGATCAAGCATCTGCGTGTGTTCTTTGTGACAGCA 624

Qy      622 GCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGT 681
            || ||||| |||||||||||  | |||||| ||||| ||  || | |||  ||| |||||
Db      625 GCCTGGAGCATCTTTGCCTATACCTGGCTTTATATAATCTTGTCTGTCAGCTCTCCTGGA 684

Qy      682 GTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTG 741
            || ||  |||| |||||||||  | || ||| |||||||||||||  | || ||  |  |
Db      685 GTTGTGGAGGTCTGGGAAGGCTTGCTTACTTTCTTCTTCTTTCCCATCTGCGTTGTGTTC 744

Qy      742 GCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACA 801
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Db      745 GCGTGGGTAGCAGACAGGCGGCTTCTCTTTTACAAGTATGTCTACAAGCGGTACAGGGCC 804

Qy      802 GACAAACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCC---------TAAGGGC 852
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Db      805 GGCAAGCAGAGGGGGATGATCATTGAACATGAAGGAGACAGACCAGCTTCCAAAACTGAA 864

Qy      853 ATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTG 912
            || || |||||||||||| || | || || ||| ||    ||         | | | |||
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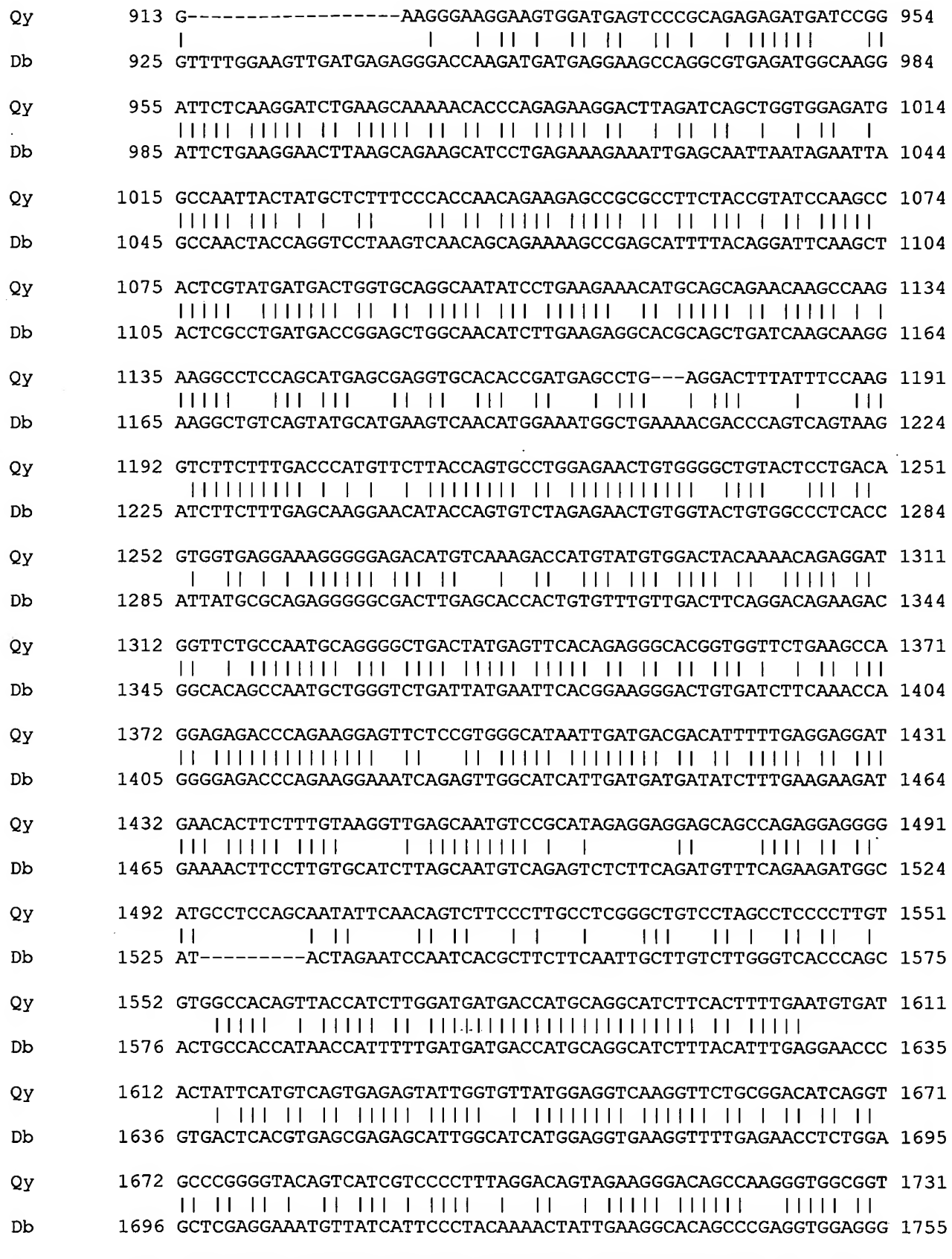

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Db       1756 GAAGACTTTGAGGACACCTGTGGAGAGCTCGAATTCCAGAACGATGAAATAGT 1808


RESULT 12
BI522813
LOCUS       BI522813                 792 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603175911F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240066 5',
            mRNA sequence.
ACCESSION   BI522813
VERSION     BI522813.1  GI:15347605
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 792)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11605  row: f  column: 03
            High quality sequence stop: 778.
FEATURES             Location/Qualifiers
     source          1. .792
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240066"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_121"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match             39.7%;  Score 739.8;  DB 4;  Length 792;
  Best Local Similarity   98.7%;  Pred. No. 1.1e-200;
  Matches  767;  Conservative    0;  Mismatches    7;  Indels    3;  Gaps    2;

Qy        993 CTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAACAGAAGAGCCG 1052
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db          1 CTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAACAGAAGAGCCG 60

Qy       1053 CGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCCTGAAGAA 1112
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCCTGAAGAA 120

Qy       1113 ACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCGATGAGCC 1172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCGATGAGCC 180

Qy       1173 TGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGGAGAACTG 1232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGGAGAACTG 240

Qy       1233 TGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCATGTATGT 1292
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Db        241 TGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCATGTATGT 300

Qy       1293 GGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCACAGAGGG 1352
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Db        301 GGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCACAGAGGG 360

Qy       1353 CACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAATTGATGA 1412
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Db        361 CACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAATTGATGA 420

Qy       1413 CGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCATAGAGGA 1472
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Db        421 CGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCATAGAGGA 480

Qy       1473 GGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGCCTCGGGC 1532
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Db        481 GGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGCCTCGGGC 540

Qy       1533 TGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATGCAGGCAT 1592
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Db        541 TGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATGCAGGCAT 600

Qy       1593 CTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGTGTTATGGAGGTCAA 1652
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Db        601 CTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGTGTTATGGAGGTCAA 660

Qy       1653 GGTTCTGCGGACATCAGGTGCCCGGGG-TACAGTCATCGTCCCCTTTAGGACAGTAGAAG 1711
              |||||||||||||||||||| ||||| ||||||||||||||||||||||||||||||||
Db        661 GGTTCTGCGGACATCAGGTGCACGGGGCTACAGTCATCGTCCCCTTTAGGACAGTAGAAG 720

Qy       1712 GGACAGCCAAGGGTGGCGGT--GAGGACTTTGAAGACACATATGGGGAGTTGGAATT 1766
              |||||||||||||||||||    ||||| |||||||||||||||||||| | | |
Db        721 GGACAGCCAAGGGTGGCGGTCGACGGACTCTGAAGACACATATGGGGAGTTTGGAAT 777
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RESULT 13
BX368185
LOCUS BX368185 916 bp mRNA linear EST 26-APR-2004
DEFINITION BX368185 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens cDNA clone CS0DD006YJ07 5-PRIME, mRNA sequence.
ACCESSION BX368185

VERSION BX368185.2 GI:46572003
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 916)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 8, 2003 this sequence version replaced gi:30445119.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7256.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0BAA006ZD07_CS00533_2&c=7256.r

FEATURES Location/Qualifiers
source 1. .916
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/db_xref="taxon:9606"
/clone="CS0DD006YJ07"
/tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
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/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Query Match 39.6%; Score 737.8; DB 5; Length 916;
Best Local Similarity 95.1%; Pred. No. 4.2e-200;
Matches 827; Conservative 0; Mismatches 33; Indels 10; Gaps 6;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db         46 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 105

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db        106 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 165

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Db        166 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 225

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 285
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Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db        286 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 345

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Db        346 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 405

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db        466 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 525

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db        526 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 585

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Db        706 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCT-CTCACTCTCTTTTTC 764

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
               |||||||||||||||||||||||||||||||| |||||||| | ||   |||   |
Db        765 -TTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGAT-AACGACTGGTTTTTACCAA--TC 820

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Db        821 ATGCCCAAAAAGTCCCG-ACAGACCAACCCGNGGGATTT----TCTAGAGACCGAGGTGC 875

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAA 870
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Db        876 CCACCCTAGGGCCTTGGGATGGTGGGAAAA 905
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RESULT 14
AK035163
LOCUS       AK035163               4374 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus 12 days embryo embryonic body between diaphragm region
            and neck cDNA, RIKEN full-length enriched library, clone:9430095C22
            product:SODIUM/CALCIUM EXCHANGER 2 PRECURSOR (NA(+)/CA(2+)-EXCHANGE
            PROTEIN 2) homolog [Rattus norvegicus], full insert sequence.
ACCESSION   AK035163
VERSION     AK035163.1  GI:26084435
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 4374)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.

FEATURES Location/Qualifiers

source 1. .4374
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/db_xref="taxon:10090"
/clone="9430095C22"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="12 days embryo"

misc_feature 281. .3046
/note="SODIUM/CALCIUM EXCHANGER 2 PRECURSOR (NA(+)/CA(2+)-EXCHANGE PROTEIN 2) homolog [Rattus norvegicus] (SWISSPROT|P48768, evidence: FASTY, 97%ID, 100%length, match=2763)
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ORIGIN

Query Match 38.1%; Score 710.4; DB 3; Length 4374;
Best Local Similarity 65.9%; Pred. No. 6.1e-192;
Matches 1092; Conservative 0; Mismatches 536; Indels 30; Gaps 3;

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Qy        136 GAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTGCCAATCTGGTACCCG 195
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Db        401 GAAGGCTGCCAAGGTTCCTACCGCTGCCAACCAGGTGTGCTGCTGCCTGTGTGGGAACCC 460

Qy        196 GAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATA 255
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Db        461 GAGGACCCATCGCTGGGCGACAAGGTTGCACGGGCCGTGGTGTACTTTGTGGCCATGGTC 520

Qy        256 TACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATC 315
              ||||||||||| || ||||| |||||||| || || || |||||||| ||||| ||||||
Db        521 TACATGTTCCTGGGTGTGTCTATCATTGCCGATCGATTTATGGCATCCATTGAGGTCATC 580

Qy        316 ACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAACCACT 375
              || ||  | ||||  ||| | || || |  ||  | ||||| || ||||||     |||
Db        581 ACATCCAAGGAGAAAGAGATCACCATCACCAAGGCAAATGGGGAGACCAGCGTGGGCACG 640

Qy        376 ATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCCTCTGCT 435
               | ||  ||||||| || || || |||||||| || || |||||||||| ||||| ||
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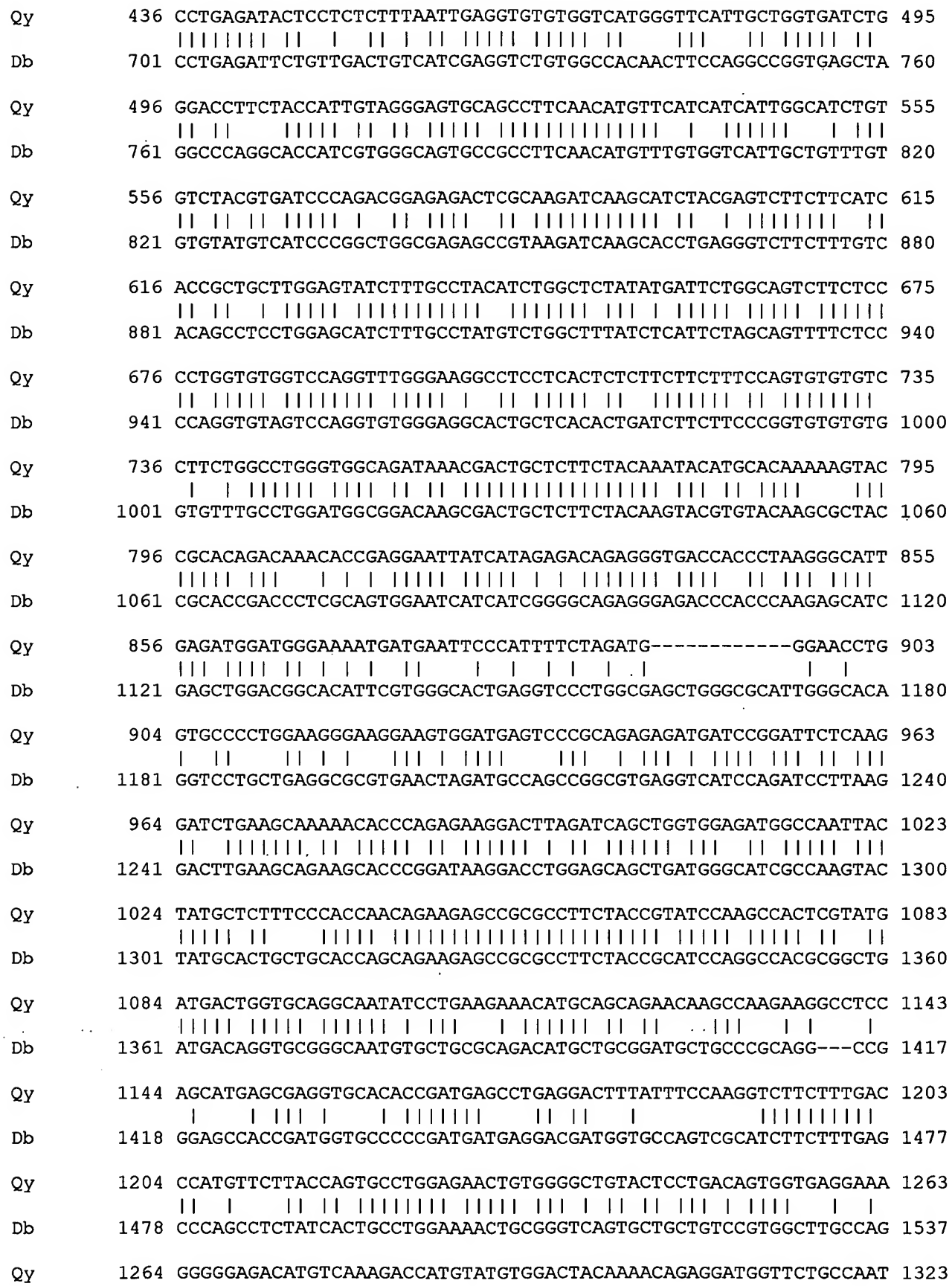

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Qy       1384 AAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTT 1443

Db       1658 AAGGACCTGCGCATCGGGATCATCGACGACGACATCTTCGAGGAGGATGAGCACTTCTTC 1717

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Db       1766 ---CCCGACGGCGGTGGGCGGCCCAAGGGGCGGCTGGTGGCGCCGCTGCTGGCCACTGTC 1822

Qy       1564 ACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTC 1623

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Qy       1624 AGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACA 1683

Db       1883 AGCGAGTGCATGGGCACTGTGGATGTGCGCGTGGTTCGCAGCTCGGGCGCCCGTGGCACT 1942

Qy       1684 GTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAA 1743

Db       1943 GTACGCCTCCCCTACCGCACAGTGGACGGCACGGCCCGTGGCGGTGGTGTACATTACGAG 2002

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RESULT 15
BX390204
LOCUS BX390204 894 bp mRNA linear EST 28-APR-2004
DEFINITION BX390204 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens cDNA clone CS0DD006YJ07 5-PRIME, mRNA sequence.
ACCESSION BX390204
VERSION BX390204.2 GI:46834875
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 894)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 8, 2003 this sequence version replaced gi:30461412.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7256.r
For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS0BAG010ZA11_CS00945_1&c=7256.r

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FEATURES             Location/Qualifiers
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                     /clone="CS0DD006YJ07"
                     /tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
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                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             38.0%;  Score 708.4;  DB 5;  Length 894;
  Best Local Similarity   93.3%;  Pred. No. 1.2e-191;
  Matches  838;  Conservative    0;  Mismatches   51;  Indels    9;  Gaps    9;

Qy         30 CTCTGCCTTCCTCCATTTTGGGCTGGTTACCTTTGTGCTCTTCCTGAATGGTCTTCGAGC 89
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Db          1 CTCTGCCTTCCTCC-TTTTGGGCTGGTTACCTTTGTGCTCTTCCTG-ATGGTCTTCGAGC 58

Qy         90 AGAGGCTGGTGGCTCAGGGGACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTTCAGG 149
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Qy        150 GTCATCGGACTGCAAGGAGGGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCT 209
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Qy        210 TGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCTTGG 269
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Qy        270 GGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAG 329
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Qy        570 AGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAG 629
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Qy        748 GTGGCAG-ATAAACGACTGCT-CTTCTACAAATACATGCACAAAAAGTACCGCACAGACA 805
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Db        779 ACCACCG-GGCACTTTCATTGAGACTGTCGTTG-CCACCCTTAGGGCACTGAGA-GGTTG 835

Qy        866 GGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGA 923
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Search completed: January 22, 2005, 17:29:22
Job time : 5799.24 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 22, 2005, 06:33:49 ; Search time 7895.51 Seconds
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11158.325 Million cell updates/sec

Title: US-10-054-680-3
Perfect score: 1863
Sequence: 1 atggcgtggttaaggttgca.....ggaaagccagtattgggtga 1863

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1863	100.0	1863	6	AX496813	AX496813 Sequence
2	1861.4	99.9	5146	9	AF510503	AF510503 Homo sapi
3	1784.6	95.8	2766	6	AX496811	AX496811 Sequence

	4	1784.6	95.8	3812	6	AX496815	AX496815 Sequence
	5	1784.4	95.8	2534	9	HSNCX22	X93017 Homo sapien
	6	1783	95.7	2781	6	AX299471	AX299471 Sequence
	7	1783	95.7	2782	6	AX476818	AX476818 Sequence
	8	1783	95.7	2837	9	HSA304853	AJ304853 Homo sapi
	9	1783	95.7	2966	6	AX480881	AX480881 Sequence
	10	1783	95.7	5250	9	AF510501	AF510501 Homo sapi
	11	1783	95.7	5268	9	AF510502	AF510502 Homo sapi
	12	1782.8	95.7	1788	6	CQ736275	CQ736275 Sequence
	13	1782.8	95.7	126512	6	AX476820	AX476820 Sequence
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	18	1546.2	83.0	4640	10	BC052435	BC052435 Mus muscu
c	19	1544.4	82.9	183707	10	AC124384	AC124384 Mus muscu
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	22	1527	82.0	4854	10	RNU53420	U53420 Rattus norv
	23	1526.8	82.0	247722	2	AC099080	AC099080 Rattus no
	24	1331.4	71.5	3838	9	HSA508602	AJ508602 Homo sapi
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	29	810.6	43.5	4087	4	BOVEXCHANG	L06438 Bos taurus
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	31	805.2	43.2	3199	4	DOGSNCE	M57523 Dog cardiac
	32	799.4	42.9	3150	4	CATSCE	L35846 Felis catus
	33	796.2	42.7	3292	4	OCU52665	U52665 Oryctolagus
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ALIGNMENTS

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AX496813
LOCUS AX496813 1863 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 3 from Patent WO02059316.
ACCESSION AX496813
VERSION AX496813.1 GI:23342336
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hilbun,E. and Friddle,C.J.
  TITLE     Human ion exchanger proteins and polynucleotides encoding the same
  JOURNAL   Patent: WO 02059316-A 3 01-AUG-2002;
            LEXICON GENETICS INC (US)
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Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Qy       1861 TGA 1863
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Db       1861 TGA 1863
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RESULT 2
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LOCUS       AF510503                5146 bp    mRNA    linear   PRI 30-OCT-2002
DEFINITION  Homo sapiens Na+/Ca2+ exchanger isoform 3 splice variant 4 (SLC8A3)
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ACCESSION   AF510503
VERSION     AF510503.1  GI:24421224
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 5146)
  AUTHORS   Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
  TITLE     The human SLC8A3 gene and the tissue-specific Na(+)/Ca(2+)
            exchanger 3 isoforms
  JOURNAL   Gene 298 (1), 1-7 (2002)
  MEDLINE   22294016
   PUBMED   12406570
REFERENCE   2  (bases 1 to 5146)
  AUTHORS   Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-MAY-2002) Department of Biology, Unv. of Padova, via
            G. Colombo, Padova, PD 35131, Italy
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             99.9%;  Score 1861.4;  DB 9;  Length 5146;
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Qy       1861 TGA 1863
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Db       2615 TGA 2617
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RESULT 3
AX496811
LOCUS AX496811 2766 bp DNA linear PAT 26-SEP-2002

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DEFINITION  Sequence 1 from Patent WO02059316.
ACCESSION   AX496811
VERSION     AX496811.1  GI:23342335
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hilbun,E. and Friddle,C.J.
  TITLE     Human ion exchanger proteins and polynucleotides encoding the same
  JOURNAL   Patent: WO 02059316-A 1 01-AUG-2002;
            LEXICON GENETICS INC (US)
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity   98.5%;  Pred. No. 0;
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Db        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Qy       1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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Db       1797 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837


RESULT 4
AX496815
LOCUS       AX496815                3812 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 5 from Patent WO02059316.
ACCESSION   AX496815
VERSION     AX496815.1  GI:23342337
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hilbun,E. and Friddle,C.J.
  TITLE     Human ion exchanger proteins and polynucleotides encoding the same
  JOURNAL   Patent: WO 02059316-A 5 01-AUG-2002;
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ORIGIN
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Query Match 95.8%; Score 1784.6; DB 6; Length 3812;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db        618 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 677

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db        678 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 737

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Db        738 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 797

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db        798 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 857

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db        858 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 917

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Db        918 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 977

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Db        978 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 1037

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db       1038 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 1097

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db       1098 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 1157

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db       1158 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 1217

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db       1218 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1277

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Db       1278 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1337

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db       1338 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1397
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Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Db       1458 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 1517

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Db       1518 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1577

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Db       1578 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1637

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Db       1638 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1697

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Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db       2298 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2357

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
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Db       2358 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 2413

Qy       1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
                | | |  || | ||| |||||||   |    |    |||||
Db       2414 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 2454


RESULT 5
HSNCX22
LOCUS       HSNCX22                 2534 bp    DNA     linear   PRI 12-NOV-2000
DEFINITION  Homo sapiens partial SCL8A3 gene for solute carrier family 8
            (sodium/calcium exchanger), member 3 (SCL8A3), exon 2.
ACCESSION   X93017
VERSION     X93017.1  GI:1067133
KEYWORDS    SLC8A3 gene; sodium-calcium exchanger.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kraev,A., Chumakov,I. and Carafoli,E.
  TITLE     The organization of the human gene NCX1 encoding the sodium-calcium
            exchanger
  JOURNAL   Genomics 37 (1), 105-112 (1996)
  MEDLINE   97079665
   PUBMED   8921376
REFERENCE   2  (bases 1 to 2534)
  AUTHORS   Kraev,A.S.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-NOV-1995) A.S. Kraev, Swiss Federal Institute of
            Technology, Laboratory of Biochemistry III, Universitaetstr. 16,
            Zurich, CH-8092, SWITZERLAND
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                     /tissue_type="lung"
                     /clone_lib="Stratagene genomic #946204"
     gene            281. .2126
                     /gene="SLC8A3"
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/product="solute carrier family 8 (sodium/calcium exchanger), member 3"
/number=2

ORIGIN

Query Match 95.8%; Score 1784.4; DB 9; Length 2534;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db        343 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 402

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 462

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 522

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db        523 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 582

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db        583 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 642

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Db        643 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 702

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Db        703 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 762

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db        763 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 822

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db        823 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 882

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db        883 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 942

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db        943 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1002

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Db       1003 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1062
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Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db       1063 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1122

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Db       1123 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 1182

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Db       1183 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 1242

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Db       1243 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1302

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Db       1303 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1362

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Db       1423 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1482

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Db       1483 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1542

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Db       1543 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1602

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Db       1843 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1902

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Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db       2023 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2082

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
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RESULT 6
AX299471
LOCUS       AX299471                2781 bp    DNA     linear   PAT 26-NOV-2001
DEFINITION  Sequence 1 from Patent WO0183744.
ACCESSION   AX299471
VERSION     AX299471.1  GI:17129228
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Wilm,C.
  TITLE     Natrium-calcium exchanger protein
  JOURNAL   Patent: WO 0183744-A 1 08-NOV-2001;
            MERCK PATENT GmbH (DE)
FEATURES             Location/Qualifiers
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ORIGIN

Query Match 95.7%; Score 1783; DB 6; Length 2781;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1812; Conservative 0; Mismatches 25; Indels 4; Gaps 1;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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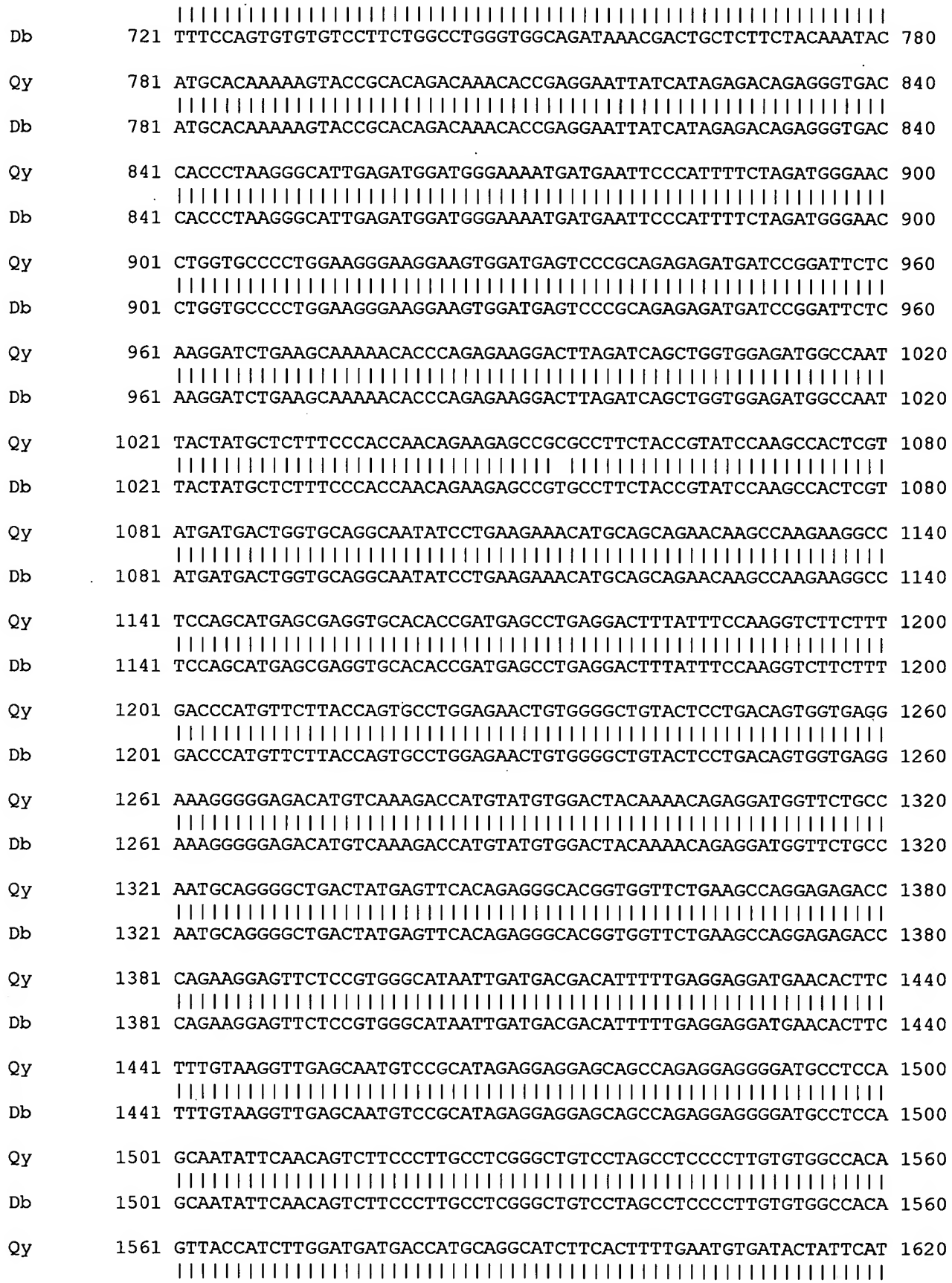

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RESULT 7
AX476818
LOCUS       AX476818               2782 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 1 from Patent WO0233086.
ACCESSION   AX476818
VERSION     AX476818.1  GI:22216098
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Merkulov,G.V., Ketchum,K.A., Shao,W., Yan,C., di Francesco,V. and
            Beasley,E.M.
  TITLE     Isolated human transporter proteins, nucleic acid molecules
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  JOURNAL   Patent: WO 0233086-A 1 25-APR-2002;
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FEATURES             Location/Qualifiers
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ORIGIN

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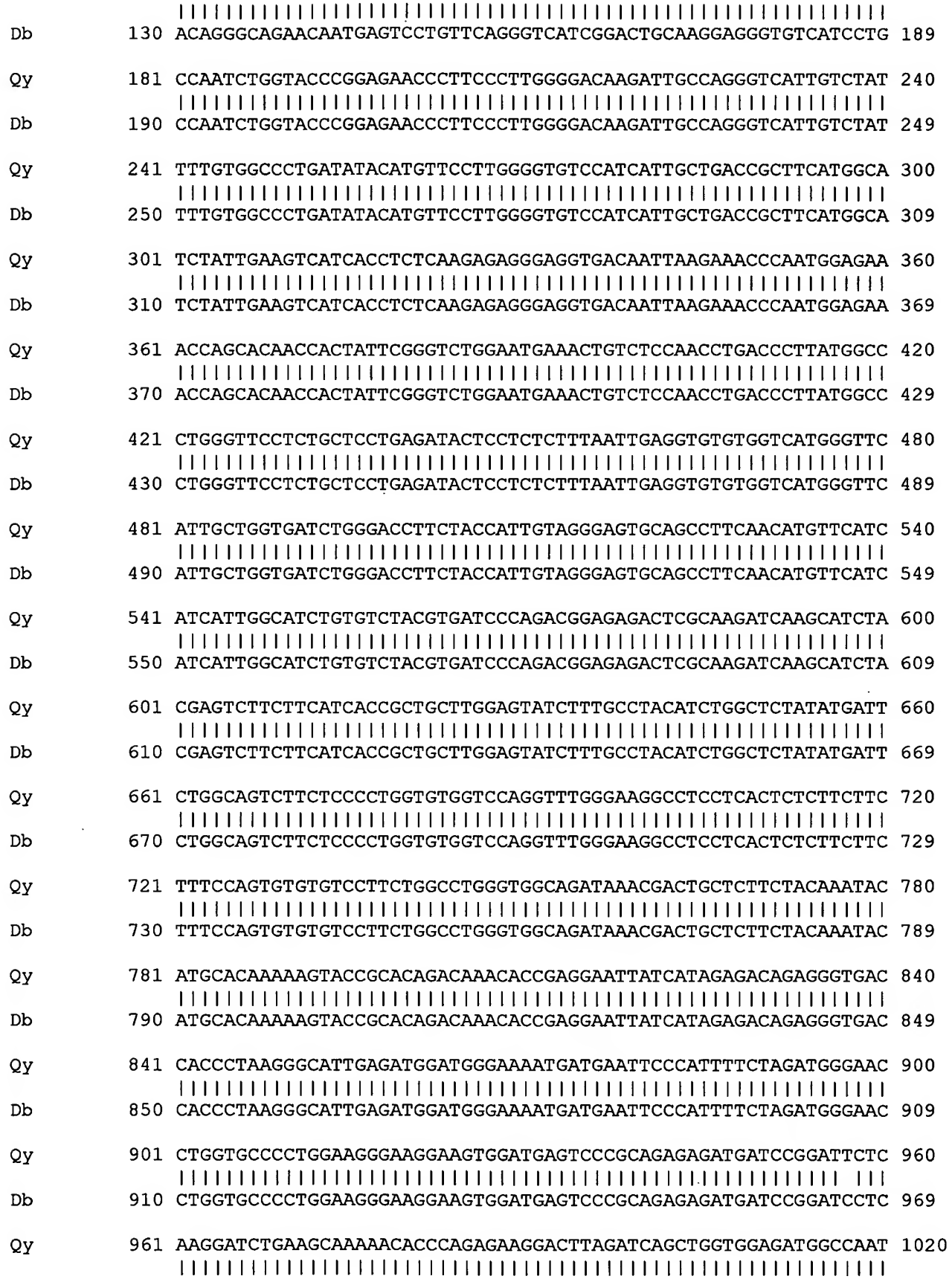

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RESULT 8
HSA304853
LOCUS HSA304853 2837 bp mRNA linear PRI 06-JUN-2001
DEFINITION Homo sapiens mRNA for sodium/calcium exchanger, SCL8A3, alternative splice form B (SCL8A3 gene).
ACCESSION AJ304853
VERSION AJ304853.1 GI:14330384
KEYWORDS alternative splicing; form B; SCL8A3 gene; SCL8A3 protein; Sodium/calcium exchanger.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Gabellini,N.
TITLE Characterization of the human SCL8A3 gene for solute carrier family 8, member 3 (sodium/calcium exchanger)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2837)
AUTHORS Bortoluzzi,S.
TITLE Direct Submission
JOURNAL Submitted (22-DEC-2000) Bortoluzzi S., Department of Biology and Department of Biological Chemistry, University of Padova, via G. Colombo 3, 35131 PADOVA, ITALY
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ORIGIN

Query Match 95.7%; Score 1783; DB 9; Length 2837;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1812; Conservative 0; Mismatches 25; Indels 4; Gaps 1;

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Db       1743 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1802

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
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Db       1803 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1858

Qy       1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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Db       1859 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1899


RESULT 9
AX480881
LOCUS       AX480881                2966 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 41 from Patent WO0246415.
ACCESSION   AX480881
VERSION     AX480881.1  GI:22217538
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Lee,E.A., Baughn,M.R., Yue,H., Ding,L., Raumann,B.E., Hafalia,A.J.,
            Khan,F.A., Nguyen,D.B., Elliott,V.S., Ramkumar,J., Walia,N.K.,
            Ison,C.H., Lu,Y., Gandhi,A.R., Warren,B.A., Duggan,B.M.,
            Tribouley,C.M., Burford,N., Lu,D.A., Lal,P.G., Yao,M.G., Xu,Y.,
            Bruns,C.M., Thangavelu,K., Swarnakar,A., Tang,Y.T., Azimzai,Y.,
            Thornton,M., Arvizu,C. and Policky,J.L.
  TITLE     Transporters and ion channels
  JOURNAL   Patent: WO 0246415-A 41 13-JUN-2002;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .2966
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ORIGIN

  Query Match             95.7%;  Score 1783;  DB 6;  Length 2966;
  Best Local Similarity   98.4%;  Pred. No. 0;
  Matches 1812;  Conservative    0;  Mismatches   25;  Indels    4;  Gaps    1;

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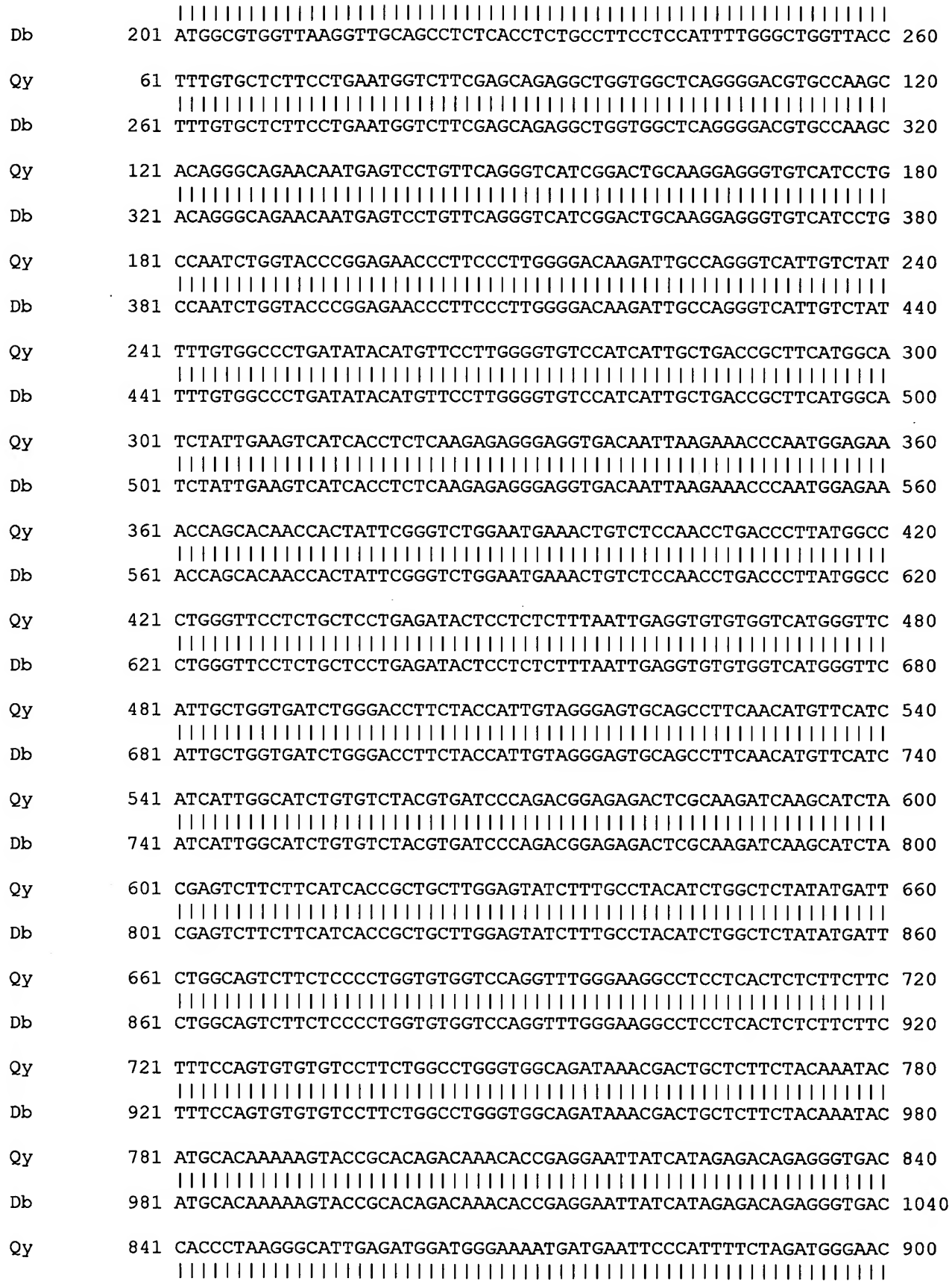

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Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Db       1221 TACTATGCTCTTTCCCACCAACAGAAGAGCCGTGCCTTCTACCGTATCCAAGCCACTCGT 1280

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Db       1341 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1400

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Qy       1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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Db       1997 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 2037
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RESULT 10
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LOCUS       AF510501                5250 bp    mRNA    linear   PRI 30-OCT-2002
DEFINITION  Homo sapiens Na+/Ca2+ exchanger isoform 3 splice variant 2 (SLC8A3)
            mRNA, complete cds; alternatively spliced.
ACCESSION   AF510501
VERSION     AF510501.1  GI:24421220
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 5250)
  AUTHORS   Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
  TITLE     The human SLC8A3 gene and the tissue-specific Na(+)/Ca(2+)
            exchanger 3 isoforms
  JOURNAL   Gene 298 (1), 1-7 (2002)
  MEDLINE   22294016
   PUBMED   12406570
REFERENCE   2  (bases 1 to 5250)
  AUTHORS   Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-MAY-2002) Department of Biology, Unv. of Padova, via
            G. Colombo, Padova, PD 35131, Italy
FEATURES             Location/Qualifiers
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     .               alternatively spliced"
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ORIGIN

  Query Match             95.7%;  Score 1783;  DB 9;  Length 5250;
  Best Local Similarity   98.4%;  Pred. No. 0;
  Matches 1812;  Conservative    0;  Mismatches   25;  Indels    4;  Gaps    1;

Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db        755 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 814

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db        815 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 874

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db        935 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 994

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Db       1115 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 1174

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db       1175 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 1234

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db       1235 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 1294

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db       1355 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1414

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db       1475 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1534

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db       2435 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2494

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Qy       1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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RESULT 11
AF510502
LOCUS       AF510502                5268 bp    mRNA    linear   PRI 30-OCT-2002
DEFINITION  Homo sapiens Na+/Ca2+ exchanger isoform 3 splice variant 3 (SLC8A3)
            mRNA, complete cds; alternatively spliced.
ACCESSION   AF510502
VERSION     AF510502.1  GI:24421222
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo..
REFERENCE   1  (bases 1 to 5268)
  AUTHORS   Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
  TITLE     The human SLC8A3 gene and the tissue-specific Na(+)/Ca(2+)
            exchanger 3 isoforms
  JOURNAL   Gene 298 (1), 1-7 (2002)
  MEDLINE   22294016
   PUBMED   12406570
REFERENCE   2  (bases 1 to 5268)
  AUTHORS   Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-MAY-2002) Department of Biology, Unv. of Padova, via
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        G. Colombo, Padova, PD 35131, Italy
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                     LIKKTNLALVVGTHSWRDQFMEAITVSAAGDEDEDESGEERLPSCFDYVMHFLTVFWK
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     3'UTR           3539. .5268
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ORIGIN

  Query Match             95.7%;  Score 1783;  DB 9;  Length 5268;
  Best Local Similarity   98.4%;  Pred. No. 0;
  Matches 1812;  Conservative    0;  Mismatches   25;  Indels    4;  Gaps    1;

Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        755 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 814

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        815 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 874

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Db        875 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 934

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Db        935 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 994

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Db       1055 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 1114

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Db       1115 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 1174

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db       1175 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 1234

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db       1235 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 1294

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db       1295 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 1354

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db       1355 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1414

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Db       1415 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1474

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db       1475 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1534

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Db       1535 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 1594

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Db       1595 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 1654

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Db       1655 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1714

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
             |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1775 TACTATGCTCTTTCCCACCAACAGAAGAGCCGTGCCTTCTACCGTATCCAAGCCACTCGT 1834

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Db       1835 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1894

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Db       1895 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1954

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Db       1955 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 2014

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Db       2135 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 2194

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2195 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 2254

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Db       2375 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 2434

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
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Db       2495 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 2550

Qy       1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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RESULT 12
CQ736275
LOCUS CQ736275 1788 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 22209 from Patent WO02068579.
ACCESSION CQ736275
VERSION CQ736275.1 GI:42330964
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
JOURNAL Patent: WO 02068579-A 22209 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES Location/Qualifiers
source 1. .1788
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 95.7%; Score 1782.8; DB 6; Length 1788;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1784; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCAGCACAACAACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Db        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

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Db        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Db        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Db        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Db        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Db       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Db       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Db       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
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RESULT 13
AX476820
LOCUS       AX476820              126512 bp    DNA     linear   PAT 12-AUG-2002
DEFINITION  Sequence 3 from Patent WO0233086.
ACCESSION   AX476820
VERSION     AX476820.1  GI:22216099
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Merkulov,G.V., Ketchum,K.A., Shao,W., Yan,C., di Francesco,V. and
            Beasley,E.M.
  TITLE     Isolated human transporter proteins, nucleic acid molecules
            encoding human transporter proteins, and uses thereof
  JOURNAL   Patent: WO 0233086-A 3 25-APR-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
     source          1. .126512
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/organism="Homo sapiens"
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ORIGIN

Query Match 95.7%; Score 1782.8; DB 6; Length 126512;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1784; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db       2250 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 2309

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Db       2310 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 2369

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db       2370 ACCAGCACAACAACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 2429

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db       2430 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 2489

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db       2490 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 2549

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2550 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 2609

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db       2610 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 2669

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Db       2670 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 2729
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Qy       721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Qy       781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Qy       841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Db      2850 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 2909

Qy       901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Qy       961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Db      2970 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 3029

Qy      1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Db      3030 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 3089

Qy      1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Db      3090 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 3149

Qy      1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Db      3150 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 3209

Qy      1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Qy      1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Qy      1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Qy      1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Qy      1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Db      3450 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 3509

Qy      1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Qy      1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
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RESULT 14
AF508982
LOCUS       AF508982               145118 bp    DNA     linear   PRI 24-OCT-2002
DEFINITION  Homo sapiens Na+/Ca2+ exchanger isoform 3 (SLC8A3) gene, promoter
            region and complete cds.
ACCESSION   AF508982
VERSION     AF508982.1  GI:22087482
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 145118)
  AUTHORS   Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
  TITLE     The human SLC8A3 gene and the tissue-specific Na+/Ca2+ exchanger 3
            isoforms
  JOURNAL   Gene 298 (1), 1-7 (2002)
REFERENCE   2  (bases 1 to 145118)
  AUTHORS   Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
  TITLE     Control of the Na+/Ca2+ exchanger 3 promoter by cAMP and Ca2+ in
            differentiating neurons
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 145118)
  AUTHORS   Gabellini,N., Bortoluzzi,S., Danieli,G.A. and Carafoli,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-MAY-2002) Department of Biology, University of
            Padova, via G. Colombo 3, Padova, PD 35131, Italy
FEATURES             Location/Qualifiers
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                     /chromosome="14"
                     /map="14q24.2"
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                     /product="Na+/Ca2+ exchanger isoform 3"
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     CDS             join(20915. .22698,128396. .128499,133522. .133539,
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                     /codon_start=1
                     /product="Na+/Ca2+ exchanger isoform 3"
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                     RTVEGTAKGGGEDFEDTYGELEFKNDETVKTIRVKIVDEEEYERQENFFIALGEPKWM
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ORIGIN
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  Query Match             95.7%;  Score 1782.8;  DB 9;  Length 145118;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1784;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      20915 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 20974

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db      20975 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 21034

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db      21215 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 21274

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Db      21275 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 21334

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db      21335 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 21394

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      21395 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 21454

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db      21455 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 21514

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db      21575 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 21634

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Db      21635 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 21694

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Db      21815 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 21874

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Db      21935 TACTATGCTCTTTCCCACCAACAGAAGAGCCGTGCCTTCTACCGTATCCAAGCCACTCGT 21994

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Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Db      22655 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGT 22700


RESULT 15
AC009607
LOCUS       AC009607               146055 bp    DNA     linear   HTG 04-MAY-2001
DEFINITION  Homo sapiens clone RP11-1I11, WORKING DRAFT SEQUENCE, 31 unordered
            pieces.
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ACCESSION AC009607
VERSION AC009607.3 GI:8072446
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 146055)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens, clone RP11-1I11
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 146055)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A., Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Depayre,E., Devon,K., Dewar,K., Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Jones,C., Kann,L., Karatas,A., Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J., Molla,M., Morris,W., Morrow,J., Mychaleckyj,J., Naylor,J., Niloff,M., O'Connor,T., O'Donnell,P., Pavlin,B., Peterson,K., Pollara,V., Riley,R., Roberts,D., Roy,A., Severy,P., Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A., Tesfaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
TITLE Direct Submission
JOURNAL Submitted (28-AUG-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On May 25, 2000 this sequence version replaced gi:7321520.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
---------- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
---------- Project Information
Center project name: L1464
Center clone name: 1_I_11
---------- Summary Statistics
Sequencing vector: M13; M77815; 99% of reads
Sequencing vector: Plasmid; n/a; %-0.f%% of reads
0.776287932251235Chemistry: Dye-primer-amersham; 6% of reads
Chemistry: Dye-terminator Big Dye; 94% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 126247 bases at least Q40
Consensus quality: 134710 bases at least Q30
Consensus quality: 138332 bases at least Q20
Insert size: 160000; agarose-fp
Insert size: 143055; sum-of-contigs
Quality coverag.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 31 contigs. The true order of the pieces
* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1166: contig of 1166 bp in length
* 1167 1266: gap of 100 bp
* 1267 2417: contig of 1151 bp in length
* 2418 2517: gap of 100 bp
* 2518 3635: contig of 1118 bp in length
* 3636 3735: gap of 100 bp
* 3736 4851: contig of 1116 bp in length
* 4852 4951: gap of 100 bp
* 4952 6701: contig of 1750 bp in length
* 6702 6801: gap of 100 bp
* 6802 8629: contig of 1828 bp in length
* 8630 8729: gap of 100 bp
* 8730 10482: contig of 1753 bp in length
* 10483 10582: gap of 100 bp
* 10583 12126: contig of 1544 bp in length
* 12127 12226: gap of 100 bp
* 12227 13831: contig of 1605 bp in length
* 13832 13931: gap of 100 bp
* 13932 16132: contig of 2201 bp in length
* 16133 16232: gap of 100 bp
* 16233 17951: contig of 1719 bp in length
* 17952 18051: gap of 100 bp
* 18052 20069: contig of 2018 bp in length
* 20070 20169: gap of 100 bp
* 20170 22565: contig of 2396 bp in length
* 22566 22665: gap of 100 bp
* 22666 24924: contig of 2259 bp in length
* 24925 25024: gap of 100 bp
* 25025 26996: contig of 1972 bp in length
* 26997 27096: gap of 100 bp
* 27097 28834: contig of 1738 bp in length
* 28835 28934: gap of 100 bp
* 28935 33803: contig of 4869 bp in length
* 33804 33903: gap of 100 bp
* 33904 38177: contig of 4274 bp in length
* 38178 38277: gap of 100 bp
* 38278 42132: contig of 3855 bp in length
* 42133 42232: gap of 100 bp
* 42233 45874: contig of 3642 bp in length
* 45875 45974: gap of 100 bp
* 45975 50807: contig of 4833 bp in length
* 50808 50907: gap of 100 bp
* 50908 55690: contig of 4783 bp in length
* 55691 55790: gap of 100 bp
* 55791 60868: contig of 5078 bp in length
* 60869 60968: gap of 100 bp
* 60969 65180: contig of 4212 bp in length
* 65181 65280: gap of 100 bp
* 65281 72495: contig of 7215 bp in length
* 72496 72595: gap of 100 bp
* 72596 79536: contig of 6941 bp in length
* 79537 79636: gap of 100 bp

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            *    86014    86113: gap of 100 bp
            *    86114    98467: contig of 12354 bp in length
            *    98468    98567: gap of 100 bp
            *    98568   112312: contig of 13745 bp in length
            *   112313   112412: gap of 100 bp
            *   112413   128733: contig of 16321 bp in length
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ORIGIN

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138694

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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138754

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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138814

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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138874

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Qy         541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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139174

Qy         601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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139234

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139294

Qy         721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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139534

Qy         961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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140014

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Search completed: January 22, 2005, 13:29:19
Job time : 7903.51 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 22, 2005, 05:47:49 ; Search time 872.539 Seconds
(without alignments)
11208.289 Million cell updates/sec

Title: US-10-054-680-3
Perfect score: 1863
Sequence: 1 atggcgtggttaaggttgca.....ggaaagccagtattgggtga 1863

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
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8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1863	100.0	1863	6	ABQ78862	Abq78862 Human ion
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3	1784.6	95.8	2766	6	ABQ78864	Abq78864 Human ion
4	1784.6	95.8	2769	6	ABQ78866	Abq78866 Human ion
5	1784.6	95.8	2769	6	ABQ78865	Abq78865 Human ion

6	1784.6	95.8	2778	12	ADH42314	Adh42314 Novel hum
7	1784.6	95.8	2778	12	ADH42306	Adh42306 Novel hum
8	1784.6	95.8	3812	6	ABQ78863	Abq78863 Human ion
9	1784.4	95.8	2534	10	ACC00414	Acc00414 Human 690
10	1783	95.7	2781	6	ABA04756	Aba04756 Human nat
11	1783	95.7	2782	6	ABN83428	Abn83428 Human tra
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13	1783	95.7	2966	6	ABZ33735	Abz33735 Human TRI
14	1782.8	95.7	126512	6	ABN83429	Abn83429 Human tra
15	1782.4	95.7	2813	8	ABX56261	Abx56261 Human NOV
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27	785.2	42.1	1836	4	AAI44657	Aai44657 Probe #13
28	785.2	42.1	1836	4	ABA31619	Aba31619 Probe #10
29	785.2	42.1	1836	4	AAK12937	Aak12937 Human bra
30	785.2	42.1	1836	4	ABS38231	Abs38231 Human liv
31	785.2	42.1	1836	6	ABS12734	Abs12734 Human gen
32	784.8	42.1	2814	4	AAH57377	Aah57377 Human hea
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43	319	17.1	24221	4	ABL09808	Abl09808 Drosophil
44	180	9.7	180	12	ACH84511	Ach84511 Human gen
45	164.2	8.8	459	4	AAI10174	Aai10174 Probe #10

ALIGNMENTS

RESULT 1
ABQ78862
ID ABQ78862 standard; cDNA; 1863 BP.
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AC ABQ78862;
XX
DT 09-OCT-2002 (first entry)
XX
DE Human ion exchanger protein #2 cDNA.
XX
KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;

KW gene; ss; chromosome 14.
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OS Homo sapiens.
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XX
PD 01-AUG-2002.
XX
PF 22-JAN-2002; 2002WO-US001817.
XX
PR 23-JAN-2001; 2001US-0263384P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Friddle CJ, Hilbun E;
XX
DR WPI; 2002-599791/64.
DR P-PSDB; ABB81914.
XX
PT Novel polynucleotides encoding human ion exchanger proteins that are
PT structurally related to mammalian sodium-calcium exchanger proteins,
PT useful for drug screening, diagnosis and in gene therapy of biological
PT disorders.
XX
PS Disclosure; Page 39-40; 42pp; English.
XX
CC The invention relates to a novel human ion exchanger protein (NHIEP),
CC that shares structural similarity with mammalian sodium-calcium exchanger
CC proteins, and potassium dependent versions of the same. The NHIEP of the
CC invention has nootropic, cytostatic, antiarthritic, and virucide
CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC or to therapeutically augment the efficacy of chemotherapeutic agents
CC used in the treatment of cancer, arthritis, or as antiviral agents. The
CC sequence encodes a NHIEP of the invention
XX
SQ Sequence 1863 BP; 464 A; 426 C; 514 G; 459 T; 0 U; 0 Other;

Query Match 100.0%; Score 1863; DB 6; Length 1863;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1863; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
```

```
Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620

Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800

Qy       1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGG 1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGG 1860
```

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Qy       1861 TGA 1863
              |||
Db       1861 TGA 1863


RESULT 2
ABQ78861
ID   ABQ78861 standard; cDNA; 2766 BP.
XX
AC   ABQ78861;
XX
DT   09-OCT-2002  (first entry)
XX
DE   Human ion exchanger protein #1 cDNA.
XX
KW   Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
KW   antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
KW   gene; ss; chromosome 14.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2766
FT                   /*tag=  a
FT                   /product= "Ion exchanger protein 1"
XX
PN   WO200259316-A2.
XX
PD   01-AUG-2002.
XX
PF   22-JAN-2002; 2002WO-US001817.
XX
PR   23-JAN-2001; 2001US-0263384P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Friddle CJ,  Hilbun E;
XX
DR   WPI; 2002-599791/64.
DR   P-PSDB; ABB81913.
XX
PT   Novel polynucleotides encoding human ion exchanger proteins that are
PT   structurally related to mammalian sodium-calcium exchanger proteins,
PT   useful for drug screening, diagnosis and in gene therapy of biological
PT   disorders.
XX
PS   Claim 1; Page 36-37; 42pp; English.
XX
CC   The invention relates to a novel human ion exchanger protein (NHIEP),
CC   that shares structural similarity with mammalian sodium-calcium exchanger
CC   proteins, and potassium dependent versions of the same. The NHIEP of the
CC   invention has nootropic, cytostatic, antiarthritic, and virucide
CC   activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC   be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC   or to therapeutically augment the efficacy of chemotherapeutic agents
CC   used in the treatment of cancer, arthritis, or as antiviral agents. The
CC   sequence encodes a NHIEP of the invention
```

XX
SQ Sequence 2766 BP; 655 A; 678 C; 760 G; 673 T; 0 U; 0 Other;

Query Match 95.8%; Score 1784.6; DB 6; Length 2766;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
             |||||||||||||||||||||||||||||||||||||    ||||| |  ||  |
Db       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1796

Qy       1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
             | | |  || | ||| |||||||   |    |    |||||
Db       1797 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837
```

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RESULT 3
ABQ78864
ID   ABQ78864 standard; cDNA; 2766 BP.
XX
AC   ABQ78864;
XX
DT   09-OCT-2002  (first entry)
XX
DE   Human ion exchanger protein #1 cDNA A/G mutant.
XX
KW   Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
KW   antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
KW   gene; ss; mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(1889,A)
FT                   /*tag=  a
XX
PN   WO200259316-A2.
XX
PD   01-AUG-2002.
XX
PF   22-JAN-2002; 2002WO-US001817.
XX
PR   23-JAN-2001; 2001US-0263384P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Friddle CJ,  Hilbun E;
XX
DR   WPI; 2002-599791/64.
XX
PT   Novel polynucleotides encoding human ion exchanger proteins that are
PT   structurally related to mammalian sodium-calcium exchanger proteins,
PT   useful for drug screening, diagnosis and in gene therapy of biological
PT   disorders.
```

XX
PS Disclosure; Page; 42pp; English.
XX
CC The invention relates to a novel human ion exchanger protein (NHIEP),
CC that shares structural similarity with mammalian sodium-calcium exchanger
CC proteins, and potassium dependent versions of the same. The NHIEP of the
CC invention has nootropic, cytostatic, antiarthritic, and virucide
CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC or to therapeutically augment the efficacy of chemotherapeutic agents
CC used in the treatment of cancer, arthritis, or as antiviral agents. The
CC sequence represents a mutant form of a NHIEP of the invention. Note: The
CC present sequence is not shown in the specification but is derived from
CC the human NHIEP sequence shown as SEQ ID 1 (ABQ78861)
XX
SQ Sequence 2766 BP; 654 A; 678 C; 761 G; 673 T; 0 U; 0 Other;

Query Match 95.8%; Score 1784.6; DB 6; Length 2766;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

```
Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
```

```
Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620

Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
                ||||||||||||||||||||||||||||||||||||||||    |||||  |  ||  |
Db       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1796

Qy       1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
                | | |  || | ||| |||||||   |    |    |||||
Db       1797 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837
```

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RESULT 4
ABQ78866
ID   ABQ78866 standard; cDNA; 2769 BP.
XX
AC   ABQ78866;
XX
DT   09-OCT-2002  (first entry)
XX
DE   Human ion exchanger protein #1 cDNA A/G+GCA mutant.
XX
KW   Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
KW   antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
KW   gene; ss; mutant.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   mutation        replace(1889,A)
FT                   /*tag=  a
FT   mutation        replace(2113. .2115,-)
FT                   /*tag=  b
XX
PN   WO200259316-A2.
XX
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PD 01-AUG-2002.
XX
PF 22-JAN-2002; 2002WO-US001817.
XX
PR 23-JAN-2001; 2001US-0263384P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Friddle CJ, Hilbun E;
XX
DR WPI; 2002-599791/64.
XX
PT Novel polynucleotides encoding human ion exchanger proteins that are
PT structurally related to mammalian sodium-calcium exchanger proteins,
PT useful for drug screening, diagnosis and in gene therapy of biological
PT disorders.
XX
PS Disclosure; Page; 42pp; English.
XX
CC The invention relates to a novel human ion exchanger protein (NHIEP),
CC that shares structural similarity with mammalian sodium-calcium exchanger
CC proteins, and potassium dependent versions of the same. The NHIEP of the
CC invention has nootropic, cytostatic, antiarthritic, and virucide
CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC or to therapeutically augment the efficacy of chemotherapeutic agents
CC used in the treatment of cancer, arthritis, or as antiviral agents. The
CC sequence represents a mutant form of a NHIEP of the invention. Note: The
CC present sequence is not shown in the specification but is derived from
CC the human NHIEP sequence shown as SEQ ID 1 (ABQ78861)
XX
SQ Sequence 2769 BP; 655 A; 679 C; 762 G; 673 T; 0 U; 0 Other;

Query Match 95.8%; Score 1784.6; DB 6; Length 2769;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620

Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
                 ||||||||||||||||||||||||||||||||||||||||    |||||  |  ||  |
Db       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1796

Qy       1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
                 | | |  || | ||| |||||||   |    |    |||||
Db       1797 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837
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RESULT 5
ABQ78865
ID ABQ78865 standard; cDNA; 2769 BP.
XX
AC ABQ78865;
XX
DT 09-OCT-2002 (first entry)
XX
DE Human ion exchanger protein #1 cDNA GCA mutant.

XX
KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
KW gene; ss; mutant.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT mutation replace(2113. .2115,-)
FT /*tag= a
XX
PN WO200259316-A2.
XX
PD 01-AUG-2002.
XX
PF 22-JAN-2002; 2002WO-US001817.
XX
PR 23-JAN-2001; 2001US-0263384P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Friddle CJ, Hilbun E;
XX
DR WPI; 2002-599791/64.
XX
PT Novel polynucleotides encoding human ion exchanger proteins that are
PT structurally related to mammalian sodium-calcium exchanger proteins,
PT useful for drug screening, diagnosis and in gene therapy of biological
PT disorders.
XX
PS Disclosure; Page; 42pp; English.
XX
CC The invention relates to a novel human ion exchanger protein (NHIEP),
CC that shares structural similarity with mammalian sodium-calcium exchanger
CC proteins, and potassium dependent versions of the same. The NHIEP of the
CC invention has nootropic, cytostatic, antiarthritic, and virucide
CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC or to therapeutically augment the efficacy of chemotherapeutic agents
CC used in the treatment of cancer, arthritis, or as antiviral agents. The
CC sequence represents a mutant form of a NHIEP of the invention. Note: The
CC present sequence is not shown in the specification but is derived from
CC the human NHIEP sequence shown as SEQ ID 1 (ABQ78861)
XX
SQ Sequence 2769 BP; 656 A; 679 C; 761 G; 673 T; 0 U; 0 Other;

Query Match 95.8%; Score 1784.6; DB 6; Length 2769;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

```
Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy       121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy       181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy       241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300

Qy       301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy       361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy       421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy       481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540

Qy       541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy       601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

Qy       661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

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Db       721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

Qy       781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Db       781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840

Qy       841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

Qy       901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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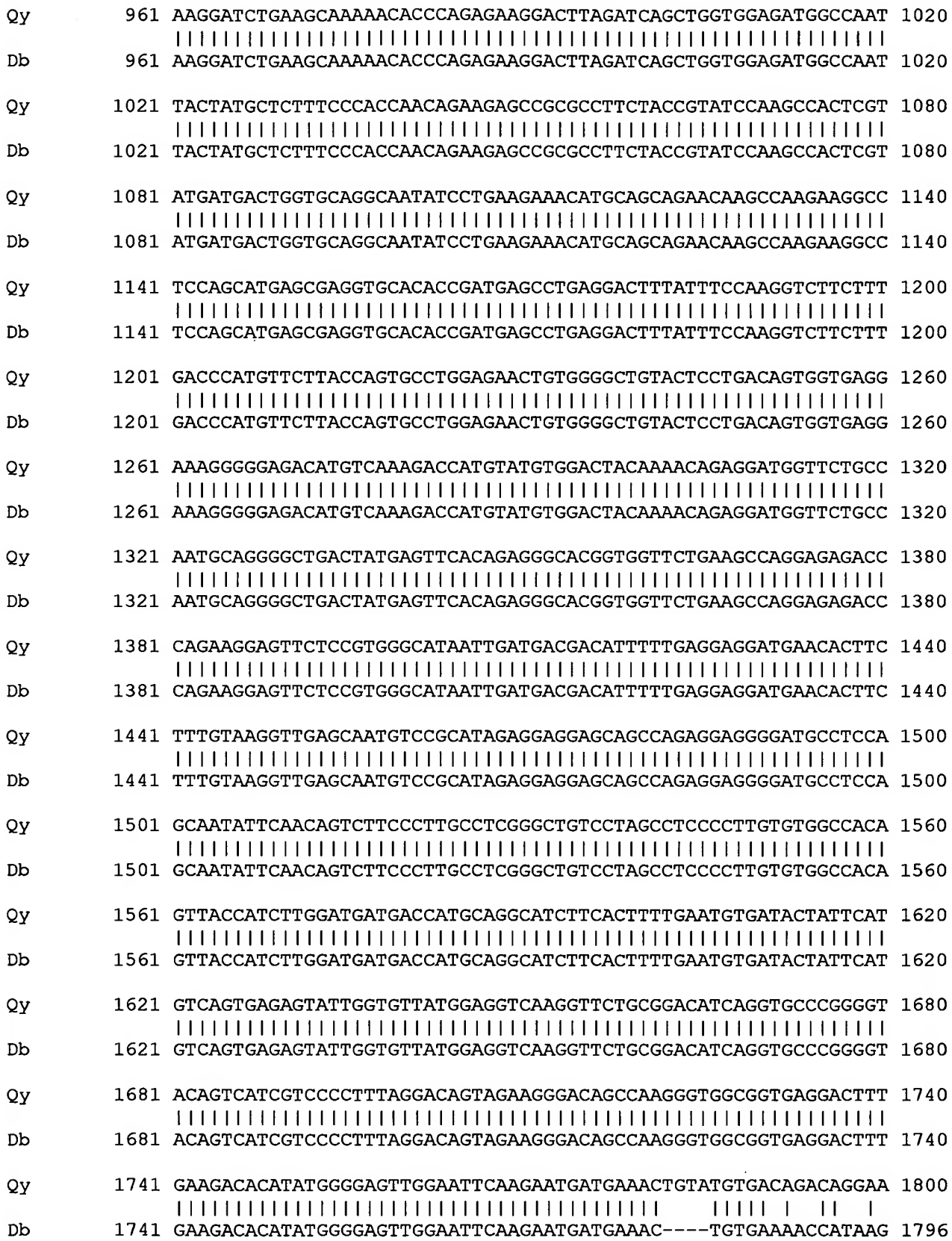
Qy 961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Db 1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
Qy 1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
Db 1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
Qy 1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
Db 1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
Qy 1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
Db 1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
Qy 1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
Db 1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
Qy 1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
Db 1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Db 1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
Qy 1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
Db 1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
Qy 1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
Db 1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
Qy 1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
Db 1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Db 1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
Qy 1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
Db 1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
Qy 1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
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Qy       1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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Db       1797 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837
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RESULT 6
ADH42314
ID ADH42314 standard; DNA; 2778 BP.
XX
AC ADH42314;
XX
DT 25-MAR-2004 (first entry)
XX
DE Novel human nucleic acid NOV55g.
XX
KW ds; gene; cardiovascular; antiarteriosclerotic; hypotensive; cytostatic;
KW anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective;
KW nootropic; antiparkinsonian; antiasthmatic; antiinfertility;
KW cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes;
KW AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's disease;
KW Parkinson's disease; asthma; fertility disorder; chromosome mapping;
KW tissue typing; preventive medicine; pharmacogenomic; vaccine.
XX
OS Homo sapiens.
XX
PN WO2003102159-A2.
XX
PD 11-DEC-2003.
XX
PF 04-JUN-2003; 2003WO-US017573.
XX
PR 04-JUN-2002; 2002US-0385490P.
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PR 12-JUN-2002; 2002US-0387934P.

PR 12-JUN-2002; 2002US-0387960P.
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PR 31-OCT-2002; 2002US-0422750P.
PR 01-NOV-2002; 2002US-0423095P.
PR 05-NOV-2002; 2002US-0423748P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Alsobrook JP, Anderson DW, Baumgartner JC, Berghs C, Boldog FL;
PI Burgess CE, Casman SJ, Catterton E, Dhanabal M, Edinger SR;
PI Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;
PI Grosse WM, Gunther E, Guo X, Gusev VY, Herrmann JL, Ji W, Kekuda R;
PI Khramtsov NV, Larochelle WJ, Li L, Liang H, Low K, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mcqueeney K, Mezick AJ, Miller CE;
PI Millet I, Padigaru M, Patturajan M, Peyman JA, Qian X, Rastelli L;
PI Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G;
PI Spytek KA, Stone DJ, Sukumaran S, Szekeres ES, Vernet CAM, Voss EZ;
PI Wolenc AR, Zhong M, Zhong H;
XX
DR WPI; 2004-053467/05.
DR P-PSDB; ADH42315.
XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, in chromosome mapping, tissue typing or in
PT pharmacogenomics.
XX
PS Claim 20; SEQ ID NO 867; 1503pp; English.
XX
CC The invention relates to 566 new isolated human polypeptides and their

CC encoding genes, sequences that are at least 95% identical to these or
CC sequences comprising one or more conservative substitutions in these. The
CC polypeptide, polynucleotide and antibodies against the polypeptides are
CC useful in diagnosing, treating or preventing NOVX-associated disorders,
CC e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
CC diabetes, AIDS, multiple sclerosis, graft-versus-host disease,
CC Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders.
CC The nucleic acids are further used as hybridization probes, in chromosome
CC mapping, tissue typing, preventive medicine, and pharmacogenomics. The
CC polypeptides are also useful as vaccines. This sequence represents an
CC example of the nucleic acid sequence of the invention.
XX
SQ Sequence 2778 BP; 656 A; 684 C; 764 G; 674 T; 0 U; 0 Other;

Query Match 95.8%; Score 1784.6; DB 12; Length 2778;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Db        370 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 429

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db        430 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 489

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db        490 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 549

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db        550 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 609
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Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Db        610 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 669

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Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db        730 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 789

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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Db        790 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 849

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Db        850 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 909

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 969

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1029

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Db       1030 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1089

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Db       1210 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1269

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Db       1330 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1389

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1390 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1449
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Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
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Db       1806 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1846
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RESULT 7
ADH42306
ID ADH42306 standard; DNA; 2778 BP.
XX
AC ADH42306;
XX
DT 25-MAR-2004 (first entry)
XX
DE Novel human nucleic acid NOV55c.
XX
KW ds; gene; cardiovascular; antiarteriosclerotic; hypotensive; cytostatic;
KW anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective;
KW nootropic; antiparkinsonian; antiasthmatic; antiinfertility;
KW cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes;
KW AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's disease;
KW Parkinson's disease; asthma; fertility disorder; chromosome mapping;
KW tissue typing; preventive medicine; pharmacogenomic; vaccine.
XX
OS Homo sapiens.
XX
PN WO2003102159-A2.
XX
PD 11-DEC-2003.
XX
PF 04-JUN-2003; 2003WO-US017573.
XX
PR 04-JUN-2002; 2002US-0385490P.
PR 04-JUN-2002; 2002US-0385615P.

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PR 05-JUN-2002; 2002US-0386041P.
PR 06-JUN-2002; 2002US-0386355P.
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PR 25-JUN-2002; 2002US-0391726P.
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XX

PA (CURA-) CURAGEN CORP.
XX
PI Alsobrook JP, Anderson DW, Baumgartner JC, Berghs C, Boldog FL;
PI Burgess CE, Casman SJ, Catterton E, Dhanabal M, Edinger SR;
PI Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;
PI Grosse WM, Gunther E, Guo X, Gusev VY, Herrmann JL, Ji W, Kekuda R;
PI Khramtsov NV, Larochelle WJ, Li L, Liang H, Low K, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mcqueeney K, Mezick AJ, Miller CE;
PI Millet I, Padigaru M, Patturajan M, Peyman JA, Qian X, Rastelli L;
PI Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G;
PI Spytek KA, Stone DJ, Sukumaran S, Szekeres ES, Vernet CAM, Voss EZ;
PI Wolenc AR, Zhong M, Zhong H;
XX
DR WPI; 2004-053467/05.
DR P-PSDB; ADH42307.
XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, in chromosome mapping, tissue typing or in
PT pharmacogenomics.
XX
PS Claim 20; SEQ ID NO 859; 1503pp; English.
XX
CC The invention relates to 566 new isolated human polypeptides and their
CC encoding genes, sequences that are at least 95% identical to these or
CC sequences comprising one or more conservative substitutions in these. The
CC polypeptide, polynucleotide and antibodies against the polypeptides are
CC useful in diagnosing, treating or preventing NOVX-associated disorders,
CC e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
CC diabetes, AIDS, multiple sclerosis, graft-versus-host disease,
CC Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders.
CC The nucleic acids are further used as hybridization probes, in chromosome
CC mapping, tissue typing, preventive medicine, and pharmacogenomics. The
CC polypeptides are also useful as vaccines. This sequence represents an
CC example of the nucleic acid sequence of the invention.
XX
SQ Sequence 2778 BP; 656 A; 684 C; 764 G; 674 T; 0 U; 0 Other;

Query Match 95.8%; Score 1784.6; DB 12; Length 2778;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 69

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 129

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 189

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 249
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Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 309

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 369

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 429

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 489

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 549

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 609

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 669

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 729

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 789

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 849

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 909

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 969

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1029

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1089
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Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1090 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1149

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1150 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1209

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1210 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1269

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1270 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1329

Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1330 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1389

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1390 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1449

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1450 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1509

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1510 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1569

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1570 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1629

Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1630 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1689

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1690 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1749

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
             ||||||||||||||||||||||||||||||||||||||||    |||||  |  ||  |
Db       1750 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1805

Qy       1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
              | | |  || | ||| |||||||   |    |    |||||
Db       1806 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1846


RESULT 8
ABQ78863
ID   ABQ78863 standard; cDNA; 3812 BP.
XX
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AC ABQ78863;
XX
DT 09-OCT-2002 (first entry)
XX
DE Human ion exchanger protein cDNA #3.
XX
KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
KW gene; ss; chromosome 14.
XX
OS Homo sapiens.
XX
PN WO200259316-A2.
XX
PD 01-AUG-2002.
XX
PF 22-JAN-2002; 2002WO-US001817.
XX
PR 23-JAN-2001; 2001US-0263384P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Friddle CJ, Hilbun E;
XX
DR WPI; 2002-599791/64.
XX
PT Novel polynucleotides encoding human ion exchanger proteins that are
PT structurally related to mammalian sodium-calcium exchanger proteins,
PT useful for drug screening, diagnosis and in gene therapy of biological
PT disorders.
XX
PS Disclosure; Page 41-42; 42pp; English.
XX
CC The invention relates to a novel human ion exchanger protein (NHIEP),
CC that shares structural similarity with mammalian sodium-calcium exchanger
CC proteins, and potassium dependent versions of the same. The NHIEP of the
CC invention has nootropic, cytostatic, antiarthritic, and virucide
CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC or to therapeutically augment the efficacy of chemotherapeutic agents
CC used in the treatment of cancer, arthritis, or as antiviral agents. The
CC sequence encodes a NHIEP of the invention, with regions of flanking
CC sequence
XX
SQ Sequence 3812 BP; 860 A; 1059 C; 1041 G; 852 T; 0 U; 0 Other;

Query Match 95.8%; Score 1784.6; DB 6; Length 3812;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        618 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 677

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 737
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Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        738 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 797

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        798 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 857

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        858 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 917

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        918 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 977

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        978 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 1037

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1038 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 1097

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1098 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 1157

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1158 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 1217

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1218 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1277

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1278 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1337

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1338 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1397

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1398 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 1457

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1458 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 1517

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1518 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1577
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Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1578 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1637

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1638 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1697

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1698 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1757

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1758 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1817

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1818 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1877

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1878 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1937

Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1938 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1997

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1998 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 2057

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2058 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 2117

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2118 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 2177

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2178 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 2237

Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2238 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 2297

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2298 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2357

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
              ||||||||||||||||||||||||||||||||||||||||    |||||  |  ||  |
Db       2358 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 2413

Qy       1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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                | | |  || | ||| |||||||   |    |    |||||
Db       2414 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 2454


RESULT 9
ACC00414
ID   ACC00414 standard; cDNA; 2534 BP.
XX
AC   ACC00414;
XX
DT   04-JUL-2003  (first entry)
XX
DE   Human 69039 coding sequence.
XX
KW   Human; 69039; neuroprotective; gene therapy; haematopoietic disorder;
KW   Na+/Ca2+ exchanger; ion transporter; neural tissue;
KW   neurological disorder; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             343. .2130
FT                   /*tag=  a
FT                   /product= "Human 69039"
XX
PN   WO2003029410-A2.
XX
PD   10-APR-2003.
XX
PF   27-SEP-2002; 2002WO-US030817.
XX
PR   28-SEP-2001; 2001US-0325737P.
XX
PA   (MILL-) MILLENIUM PHARM INC.
XX
PI   Carroll JM;
XX
DR   WPI; 2003-381617/36.
DR   P-PSDB; ABR40134.
XX
PT   Identifying a nucleic acid molecule associated with a disorder for
PT   preparing a composition for treating hematopoietic or neurological
PT   disorder by detecting the presence of a nucleic acid molecule in the
PT   sample that is amplified.
XX
PS   Claim 1; Page 109-110; 133pp; English.
XX
CC   The present sequence is the coding sequence for human 69039, a novel
CC   Na+/Ca2+ exchanger family member (ion transporter). 69039 was shown to be
CC   expressed in human haematopoietic cells, e.g. CD34-expressing progenitor
CC   cells as well as in neural tissues, e.g. brain cortex and hypothalamus.
CC   69039 may therefore be used for preparing a composition for treating
CC   haematopoietic or neurological disorder
XX
SQ   Sequence 2534 BP; 602 A; 595 C; 644 G; 693 T; 0 U; 0 Other;

  Query Match             95.8%;  Score 1784.4;  DB 10;  Length 2534;
```

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  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1785;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 402

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 462

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 522

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 582

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        583 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 642

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 702

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        703 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 762

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        763 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 822

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        823 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 882

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        883 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 942

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        943 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1002

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1003 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1062

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1122

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1123 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 1182

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1183 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 1242

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Db       1243 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1302

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1303 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1362

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Db       1363 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1422

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Db       1603 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1662

Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Db       1663 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1722

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1723 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1782

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1963 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 2022
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Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2023 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2082

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
             ||||||||||||||||||||||||||||||||||||||||||| |
Db       2083 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGT 2128
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RESULT 10
ABA04756
ID ABA04756 standard; cDNA; 2781 BP.
XX
AC ABA04756;
XX
DT 25-FEB-2002 (first entry)
XX
DE Human natrium(+)-calcium(2+) exchanger form 3 protein, HNCX3, cDNA.
XX
KW Human; Natrium(+)-Calcium(2+) exchanger form 3; HNCX3; chromosome 14;
KW cardiac failure; myocardial infarction; cardiac hypertrophy; arrhythmia;
KW myocarditis; pulmonary hypertension; cardiotoxicity; cardiant; Vaccine;
KW coronary heart disease; renal failure; ischaemic disorder;
KW Antiarrhythmic; Vasotropic; Hypotensive; cardiovascular disorder; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1. .2781
FT   /*tag= a
FT   /partial
FT   /product= "Human natrium(+)-calcium(2+) exchanger form 3
FT   protein, HNCX3"
FT   /note= "No stop codon given"
XX
PN WO200183744-A2.
XX
PD 08-NOV-2001.
XX
PF 30-APR-2001; 2001WO-EP004886.
XX
PR 02-MAY-2000; 2000EP-00109080.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Wilm C;
XX
DR WPI; 2002-041493/05.
DR P-PSDB; AAM47745.
XX
PT New polypeptide, useful as vaccines for inducing immune response against
PT diseases such as myocardial infarction, arrhythmia, ischemic disorders,
PT renal disorders in mammal.
XX
PS Claim 4; Page 34-38; 41pp; English.
XX

CC The present sequence is the coding sequence for human Natrium(+)-Calcium
CC (2+) exchanger form 3 (HNCX3). The HNCX3 gene maps to human chromosome
CC 14. HNCX3 and its coding sequence are useful for treating acute and
CC chronic cardiac failure of different aetiologies, myocardial infarction,
CC cardiac hypertrophy, arrhythmia, myocarditis, pulmonary hypertension,
CC cardiotoxicity (e.g. induced by chemotherapy), coronary heart disease,
CC acute and chronic renal failure, ischaemic disorders of skeletal muscle
CC and ischaemic brain disorders of different aetiologies
XX
SQ Sequence 2781 BP; 658 A; 678 C; 765 G; 680 T; 0 U; 0 Other;

Query Match 95.7%; Score 1783; DB 6; Length 2781;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1812; Conservative 0; Mismatches 25; Indels 4; Gaps 1;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGTGCCTTCTACCGTATCCAAGCCACTCGT 1080

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Db       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
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Db       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
             ||||||||||||||||||||||||||||||||||||||||    |||||  |  ||  |
Db       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1796

Qy       1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
             | | |  || | ||| |||||||   |    |    |||||
Db       1797 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837
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RESULT 11
ABN83428
ID   ABN83428 standard; cDNA; 2782 BP.
XX
AC   ABN83428;
XX
DT   21-AUG-2002  (first entry)
XX
DE   Human transporter protein coding sequence.
XX
KW   Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;
KW   spleen; testis; leukocyte; foetal brain; chromosome 14; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             10. .2775
FT                   /*tag=  a
FT                   /product= "Human transporter"
XX
PN   WO200233086-A2.
XX
PD   25-APR-2002.
XX
PF   17-OCT-2001; 2001WO-US032152.
XX
PR   17-OCT-2000; 2000US-0240836P.
PR   13-MAR-2001; 2001US-00804474.
XX
PA   (PEKE ) PE CORP NY.
XX
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PI Merkulov GV, Ketchum KA, Shao W, Yan C, Di Francesco V;
PI Beasley EM;
XX
DR WPI; 2002-479677/51.
DR P-PSDB; ABB83246.
XX
PT Human transporter peptide related to sodium/calcium exchanger subfamily
PT for identifying modulators useful for treating a disease or condition
PT mediated by human transporter protein.
XX
PS Claim 4; Fig 1; 200pp; English.
XX
CC The present sequence is the coding sequence of a human transporter
CC protein, which is related to the sodium/calcium exchanger subfamily.
CC Experimental data indicates expression of the transporter gene in humans
CC in brain, heart, kidney, lung, spleen, testis, leukocyte and foetal
CC brain. The gene of the transporter was mapped to chromosome 14 by ePCR
XX
SQ Sequence 2782 BP; 655 A; 685 C; 766 G; 676 T; 0 U; 0 Other;

Query Match 95.7%; Score 1783; DB 6; Length 2782;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1812; Conservative 0; Mismatches 25; Indels 4; Gaps 1;

```
Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 69

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 129

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 189

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 249

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 309

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Db        310 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 369

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Db        370 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 429

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db        430 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 489

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db 490 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 549
Qy 541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Qy 601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
Db 610 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 669
Qy 661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
Db 670 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 729
Qy 721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
Db 730 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 789
Qy 781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
Db 790 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 849
Qy 841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
Db 850 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 909
Qy 901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
Db 910 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATCCTC 969
Qy 961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
Db 970 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1029
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Db 1030 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1089
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Db 1090 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1149
Qy 1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
Db 1150 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1209
Qy 1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
Db 1210 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1269
Qy 1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
Db 1270 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1329
Qy 1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

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Db       1330 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1389

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db       1690 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1749

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
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Db       1750 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1805

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Db       1806 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1846
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RESULT 12
ADH42302
ID   ADH42302 standard; DNA; 2828 BP.
XX
AC   ADH42302;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Novel human nucleic acid NOV55a.
XX
KW   ds; gene; cardiovascular; antiarteriosclerotic; hypotensive; cytostatic;
KW   anorectic; antidiabetic; immunosuppressive; anti-HIV; neuroprotective;
KW   nootropic; antiparkinsonian; antiasthmatic; antiinfertility;
KW   cardiomyopathy; atherosclerosis; hypertension; cancer; obesity; diabetes;
KW   AIDS; multiple sclerosis; graft-versus-host disease; Alzheimer's disease;
KW   Parkinson's disease; asthma; fertility disorder; chromosome mapping;
KW   tissue typing; preventive medicine; pharmacogenomic; vaccine.
XX
OS   Homo sapiens.
XX
PN   WO2003102159-A2.
XX
```

PD 11-DEC-2003.
XX
PF 04-JUN-2003; 2003WO-US017573.
XX
PR 04-JUN-2002; 2002US-0385490P.
PR 04-JUN-2002; 2002US-0385615P.
PR 04-JUN-2002; 2002US-0385755P.
PR 05-JUN-2002; 2002US-0386041P.
PR 06-JUN-2002; 2002US-0386355P.
PR 06-JUN-2002; 2002US-0386357P.
PR 06-JUN-2002; 2002US-0386447P.
PR 06-JUN-2002; 2002US-0386459P.
PR 06-JUN-2002; 2002US-0386465P.
PR 06-JUN-2002; 2002US-0386864P.
PR 07-JUN-2002; 2002US-0386701P.
PR 07-JUN-2002; 2002US-0386796P.
PR 07-JUN-2002; 2002US-0386931P.
PR 07-JUN-2002; 2002US-0387078P.
PR 07-JUN-2002; 2002US-0387081P.
PR 07-JUN-2002; 2002US-0387083P.
PR 10-JUN-2002; 2002US-0387429P.
PR 10-JUN-2002; 2002US-0387540P.
PR 10-JUN-2002; 2002US-0387866P.
PR 11-JUN-2002; 2002US-0387606P.
PR 11-JUN-2002; 2002US-0387610P.
PR 11-JUN-2002; 2002US-0387659P.
PR 11-JUN-2002; 2002US-0387668P.
PR 11-JUN-2002; 2002US-0387696P.
PR 11-JUN-2002; 2002US-0387859P.
PR 12-JUN-2002; 2002US-0387934P.
PR 12-JUN-2002; 2002US-0387960P.
PR 12-JUN-2002; 2002US-0388022P.
PR 12-JUN-2002; 2002US-0388096P.
PR 12-JUN-2002; 2002US-0388432P.
PR 12-JUN-2002; 2002US-0388479P.
PR 13-JUN-2002; 2002US-0389123P.
PR 14-JUN-2002; 2002US-0389120P.
PR 14-JUN-2002; 2002US-0389146P.
PR 17-JUN-2002; 2002US-0389742P.
PR 18-JUN-2002; 2002US-0389604P.
PR 18-JUN-2002; 2002US-0389884P.
PR 19-JUN-2002; 2002US-0390006P.
PR 19-JUN-2002; 2002US-0390144P.
PR 19-JUN-2002; 2002US-0390209P.
PR 25-JUN-2002; 2002US-0391726P.
PR 06-AUG-2002; 2002US-0401628P.
PR 09-AUG-2002; 2002US-0402268P.
PR 12-AUG-2002; 2002US-0402822P.
PR 13-AUG-2002; 2002US-0403458P.
PR 15-AUG-2002; 2002US-0403617P.
PR 15-AUG-2002; 2002US-0403732P.
PR 26-AUG-2002; 2002US-0406182P.
PR 12-SEP-2002; 2002US-0410085P.
PR 13-SEP-2002; 2002US-0410505P.
PR 23-SEP-2002; 2002US-0412955P.
PR 30-SEP-2002; 2002US-0415195P.
PR 23-OCT-2002; 2002US-0420627P.

PR 23-OCT-2002; 2002US-0420718P.
PR 24-OCT-2002; 2002US-0420852P.
PR 31-OCT-2002; 2002US-0422750P.
PR 01-NOV-2002; 2002US-0423095P.
PR 05-NOV-2002; 2002US-0423748P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Alsobrook JP, Anderson DW, Baumgartner JC, Berghs C, Boldog FL;
PI Burgess CE, Casman SJ, Catterton E, Dhanabal M, Edinger SR;
PI Ellerman K, Ettenberg S, Gangolli EA, Gerlach VL, Gorman L;
PI Grosse WM, Gunther E, Guo X, Gusev VY, Herrmann JL, Ji W, Kekuda R;
PI Khramtsov NV, Larochelle WJ, Li L, Liang H, Low K, Macdougall JR;
PI Maclachlan T, Malyankar UM, Mcqueeney K, Mezick AJ, Miller CE;
PI Millet I, Padigaru M, Patturajan M, Peyman JA, Qian X, Rastelli L;
PI Rieger DK, Rothenberg ME, Shenoy SG, Shimkets RA, Smithson G;
PI Spytek KA, Stone DJ, Sukumaran S, Szekeres ES, Vernet CAM, Voss EZ;
PI Wolenc AR, Zhong M, Zhong H;
XX
DR WPI; 2004-053467/05.
DR P-PSDB; ADH42303.
XX
PT New NOVX polypeptides and nucleic acid molecules useful for preventing or
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,
PT atherosclerosis or diabetes, in chromosome mapping, tissue typing or in
PT pharmacogenomics.
XX
PS Claim 20; SEQ ID NO 855; 1503pp; English.
XX
CC The invention relates to 566 new isolated human polypeptides and their
CC encoding genes, sequences that are at least 95% identical to these or
CC sequences comprising one or more conservative substitutions in these. The
CC polypeptide, polynucleotide and antibodies against the polypeptides are
CC useful in diagnosing, treating or preventing NOVX-associated disorders,
CC e.g. cardiomyopathy, atherosclerosis, hypertension, cancer, obesity,
CC diabetes, AIDS, multiple sclerosis, graft-versus-host disease,
CC Alzheimer's disease, Parkinson's disease, asthma, or fertility disorders.
CC The nucleic acids are further used as hybridization probes, in chromosome
CC mapping, tissue typing, preventive medicine, and pharmacogenomics. The
CC polypeptides are also useful as vaccines. This sequence represents an
CC example of the nucleic acid sequence of the invention.
XX
SQ Sequence 2828 BP; 670 A; 692 C; 778 G; 688 T; 0 U; 0 Other;

Query Match 95.7%; Score 1783; DB 12; Length 2828;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1812; Conservative 0; Mismatches 25; Indels 4; Gaps 1;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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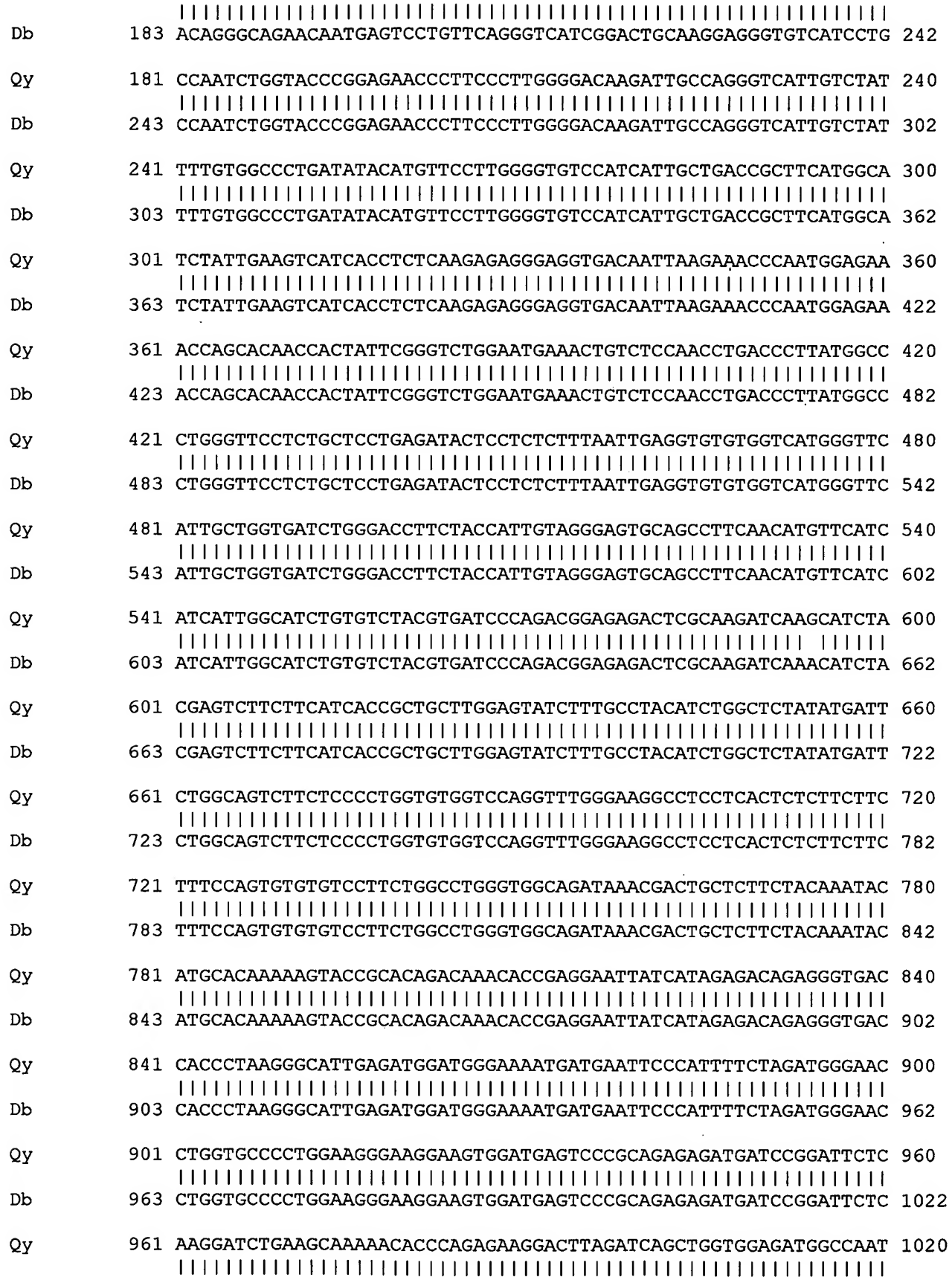

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Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Db       1083 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1142

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Db       1143 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1202

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Db       1203 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1262

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Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Db       1383 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1442

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Db       1563 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1622

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Db       1623 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1682

Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
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Db       1803 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1858

Qy       1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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Db       1859 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1899
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RESULT 13
ABZ33735
ID ABZ33735 standard; cDNA; 2966 BP.
XX
AC ABZ33735;
XX
DT 30-JAN-2003 (first entry)
XX
DE Human TRICH encoding cDNA SEQ ID NO 41.
XX
KW Human; TRICH; transporter and ion channel; transport disorder;
KW cystic fibrosis; diabetes mellitus; Parkinson's disease; cancer;
KW neurological disorder; Alzheimer's disease; Huntington's disease;
KW immunological disorder; AIDS; asthma; cell proliferative disorder;
KW transgenic; gene therapy; neuroprotective; antidiabetic; cytostatic;
KW antiparkinsonian; hypotensive; nootropic; antianaemic; anticonvulsant;
KW cerebroprotective; cardiant; anti-HIV; human immunodeficiency virus;
KW antiasthmatic; antiatherosclerotic; antigout; antiarteriosclerotic;
KW hepatotropic; antiinflammatory; virucide; cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200246415-A2.
XX
PD 13-JUN-2002.
XX
PF 05-DEC-2001; 2001WO-US046963.
XX
PR 08-DEC-2000; 2000US-0254303P.
PR 15-DEC-2000; 2000US-0256190P.
PR 21-DEC-2000; 2000US-0257504P.
PR 12-JAN-2001; 2001US-0261546P.
PR 19-JAN-2001; 2001US-0262832P.
PR 26-JAN-2001; 2001US-0264377P.
PR 02-FEB-2001; 2001US-0266019P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lee EA, Baughn MR, Yue H, Ding L, Raumann BE, Hafalia AJA;
PI Khan FA, Nguyen DB, Elliott VS, Ramkumar J, Walia NK, Ison CH;
PI Lu Y, Gandhi AR, Warren BA, Duggan BM, Tribouley CM, Burford N;
PI Lu DAM, Lal PG, Yao MG, Xu Y, Bruns CM, Thangavelu K, Swarnakar A;
PI Tang YT, Azimzai Y, Thornton M, Arvizu C, Policky JL;
XX
DR WPI; 2002-519667/55.
DR P-PSDB; ABP74104.
XX
PT Novel human transporter and ion channel polypeptide, useful in diagnosis,
PT prevention or treatment of transport, neurological, muscle, immunological
PT and cell proliferative disorders.
XX
PS Claim 96; SEQ ID NO 41; 146pp + Sequence Listing; English.
XX
CC The invention relates to human transporter and ion channel polypeptide
CC (TRICH) (I) selected from one of 32 polypeptide sequences (ABP74096-

CC ABP74127), a naturally occurring polypeptide comprising a sequence having
CC at least sequence 90 % identity to (I) or a biologically active or
CC immunogenic fragment of (I). (I) is useful for screening a compound for
CC effectiveness as an agonist or antagonist, for screening a compound that
CC specifically binds (I) or modulates the activity of (I) and for preparing
CC a polyclonal or monoclonal antibody by hybridoma technology.
CC Polynucleotides (II, ABZ33727-ABZ33758) encoding (I) are useful for
CC screening a compound altering gene expression. (I) and (II) are useful in
CC a diagnostic tests for a condition or a disease associated with the
CC expression of TRICH in a biological sample, especially disorders selected
CC from a transport disorder such as cystic fibrosis, diabetes mellitus,
CC Parkinson's disease, cardiac disorders, neurological disorders such as
CC Alzheimer's disease, Huntington's disease, muscle disorders,
CC immunological disorder such as AIDS, asthma and atherosclerosis, and cell
CC proliferative disorder such as arteriosclerosis, cirrhosis, hepatitis and
CC cancer. (II) is useful for creating knock-in humanised animals or
CC transgenic animals to model human diseases, in somatic or germline gene
CC therapy, to generate a transcript image of a tissue or cell type, for
CC detecting differences in the chromosomal location due to translocation,
CC inversion among normal, carrier or affected individuals and for mapping
CC genomic sequences. Note: The sequence data for this patent is not
CC represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX
SQ Sequence 2966 BP; 692 A; 725 C; 809 G; 740 T; 0 U; 0 Other;

Query Match 95.7%; Score 1783; DB 6; Length 2966;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1812; Conservative 0; Mismatches 25; Indels 4; Gaps 1;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db        201 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 260

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db        261 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 320

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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```
Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db        621 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 680

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db        681 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 740

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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RESULT 14
ABN83429
ID ABN83429 standard; DNA; 126512 BP.
XX
AC ABN83429;
XX
DT 21-AUG-2002 (first entry)
XX
DE Human transporter protein gene.
XX
KW Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;
KW spleen; testis; leukocyte; foetal brain; chromosome 14; gene;
KW single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX

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Query Match 95.7%; Score 1782.8; DB 6; Length 126512;
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Matches 1784; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 15
ABX56261
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XX
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XX
DT 19-FEB-2003 (first entry)
XX
DE Human NOV1a CG56258-01 DNA SEQ ID 1.
XX
KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
KW antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer; gene;
KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;
KW metabolic syndrome X; wasting disease; ds.
XX
OS Homo sapiens.
XX
PN WO200281625-A2.
XX
PD 17-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010366.
XX
PR 03-APR-2001; 2001US-0281086P.
PR 05-APR-2001; 2001US-0281906P.
PR 06-APR-2001; 2001US-0282020P.
PR 10-APR-2001; 2001US-0282930P.

PR 12-APR-2001; 2001US-0283444P.
PR 12-APR-2001; 2001US-0283512P.
PR 13-APR-2001; 2001US-0283657P.
PR 13-APR-2001; 2001US-0283678P.
PR 13-APR-2001; 2001US-0283710P.
PR 17-APR-2001; 2001US-0284234P.
PR 19-APR-2001; 2001US-0285325P.
PR 20-APR-2001; 2001US-0285381P.
PR 24-APR-2001; 2001US-0286068P.
PR 25-APR-2001; 2001US-0286292P.
PR 07-JUN-2001; 2001US-0296692P.
PR 26-JUN-2001; 2001US-0300883P.
PR 08-AUG-2001; 2001US-0311003P.
PR 13-AUG-2001; 2001US-0311973P.
PR 16-AUG-2001; 2001US-0312901P.
PR 14-SEP-2001; 2001US-0322283P.
PR 05-OCT-2001; 2001US-0327448P.
PR 31-DEC-2001; 2001US-0345734P.
PR 03-JAN-2002; 2002US-0345755P.
PR 04-FEB-2002; 2002US-0354391P.
PR 02-APR-2002; 2002US-00114153.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Padigaru M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD;
PI Smithson G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L;
PI Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA;
PI Malyankar UM, Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J;
PI Peyman JA, Catterton E, Macdougall JR, Edinger SR, Stone DJ;
PI Mazur A;
XX
DR WPI; 2003-046862/04.
DR P-PSDB; ABU12041.
XX
PT New isolated NOVX polypeptide useful for treating cardiomyopathy,
PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious
PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
PT cancer.
XX
PS Claim 3; Page 83-84; 425pp; English.
XX
CC This invention describes novel polypeptides, termed NOVX which have
CC antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,
CC neuroprotective, antiparkinsonian, antilipaemic, cytostatic, nootropic,
CC cardiant and immunomodulatory activity. The polypeptide and any
CC antibodies generated from it are useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease
CC selected from a pathology associated with the NOVX polypeptide. Fragments
CC and portions of the polynucleotides encoding NOVX polypeptides are useful
CC to map the location of NOVX genes on a chromosome, to identify
CC individuals from minute biological samples, as DNA markers for
CC restriction fragment length polymorphism (RFLP), and are useful to
CC prepare polymerase chain reaction primers. The products of the invention
CC can be used in gene therapy and for treating cardiomyopathy, metabolic
CC disorders, diabetes, atherosclerosis, obesity, infectious disease,
CC anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's
CC disease, immune disorders, haematopoietic disorders, and various

CC dyslipidaemias, metabolic disturbances associated with obesity, metabolic
CC syndrome X and wasting disorders associated with chronic diseases and
CC various cancers. ABX56261-ABX56306 represent the polynucleotide fragments
CC which encode the NOVX polypeptides represented in ABU12041-ABU12086
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SQ Sequence 2813 BP; 617 A; 716 C; 813 G; 667 T; 0 U; 0 Other;

Query Match 95.7%; Score 1782.4; DB 8; Length 2813;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1783; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Searched: 824507 seqs, 355394441 residues

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Maximum DB seq length: 2000000000

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	1	71.6	3.8	1935	4	US-09-701-068-3	Sequence 3, Appli
	2	71.6	3.8	1950	4	US-09-701-068-1	Sequence 1, Appli
	3	51.6	2.8	7218	1	US-08-232-463-14	Sequence 14, Appl
c	4	51	2.7	7218	1	US-08-232-463-14	Sequence 14, Appl
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	6	38.4	2.1	160	1	US-08-182-175A-44	Sequence 44, Appl
	7	38.4	2.1	160	1	US-08-474-633A-53	Sequence 53, Appl
	8	38.4	2.1	160	4	US-08-823-771-53	Sequence 53, Appl
	9	38.4	2.1	160	5	PCT-US92-06412-44	Sequence 44, Appl
c	10	38.4	2.1	2777	3	US-09-310-463-3	Sequence 3, Appli
c	11	38.4	2.1	2777	4	US-08-842-248A-3	Sequence 3, Appli

c	12	37.4	2.0	289	3	US-09-007-005-17	Sequence 17, Appl
c	13	37.4	2.0	289	3	US-09-244-796-17	Sequence 17, Appl
c	14	37.2	2.0	1320	4	US-09-148-545-110	Sequence 110, App
	15	37	2.0	740	4	US-09-270-767-31616	Sequence 31616, A
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	19	36.8	2.0	160	1	US-08-182-175A-34	Sequence 34, Appl
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	26	36.8	2.0	187	1	US-08-182-175A-90	Sequence 90, Appl
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c	37	36	1.9	1312	4	US-10-140-002-397	Sequence 397, App
c	38	36	1.9	1328	4	US-09-599-360B-46	Sequence 46, Appl
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	44	35.6	1.9	306	3	US-09-461-697-203	Sequence 203, App
	45	35.6	1.9	696	3	US-09-461-697-193	Sequence 193, App

ALIGNMENTS

RESULT 1
US-09-701-068-3
; Sequence 3, Application US/09701068
; Patent No. 6677506
; GENERAL INFORMATION:
; APPLICANT: Galil, Gad et al.
; TITLE OF INVENTION: DNA CODING FOR A Mg2+/H+ OR Zn2+/H+ EXCHANGER AND TRANSGENIC PLANTS
; TITLE OF INVENTION: EXPRESSING SAME
; FILE REFERENCE: 01/21317
; CURRENT APPLICATION NUMBER: US/09/701,068
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1935
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana

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;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (136)..(1755)
US-09-701-068-3

  Query Match             3.8%;  Score 71.6;  DB 4;  Length 1935;
  Best Local Similarity   48.2%;  Pred. No. 6.4e-12;
  Matches  268;  Conservative    0;  Mismatches  279;  Indels    9;  Gaps    2;

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Qy        343 AAGAAACCCAATGGAGAAACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCC 402
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Qy        517 AGTGCAGCCTTCAACATGTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGA 576
                || || ||  |  | ||| ||||   |   | ||||||   |||      ||  |||
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Qy        577 GAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTT 636
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RESULT 2
US-09-701-068-1
; Sequence 1, Application US/09701068
; Patent No. 6677506
; GENERAL INFORMATION:
;  APPLICANT: Galil, Gad et al.
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; TITLE OF INVENTION: DNA CODING FOR A Mg2+/H+ OR Zn2+/H+ EXCHANGER AND TRANSGENIC PLANTS
; TITLE OF INVENTION: EXPRESSING SAME
; FILE REFERENCE: 01/21317
; CURRENT APPLICATION NUMBER: US/09/701,068
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1950
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-701-068-1

Query Match 3.8%; Score 71.6; DB 4; Length 1950;
Best Local Similarity 48.2%; Pred. No. 6.4e-12;
Matches 268; Conservative 0; Mismatches 279; Indels 9; Gaps 2;

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Db        438 GACATCAGTTTGTTGGCGTTTGGAACTAGCTTCCCTCAGATTTCTTTGGCTACCATCGAT 497

Qy        463 GTGTGTGGTCAT------GGGTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGG 516
              |      |  ||      | |     |||||| | ||| || |||   ||  |||| ||
Db        498 GCAATACGGAATATGGGGGAGCGGTATGCTGGAGGTCTTGGTCCTGGAACACTTGTTGGC 557

Qy        517 AGTGCAGCCTTCAACATGTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGA 576
                || || ||  |  | |||  ||||   |   | ||||||  |||     ||  |||
Db        558 TCAGCTGCATTTGATCTTTTCCCCATCCACGCTGTTTGTGTCGTTGTGCCAAAAGCTGGA 617

Qy        577 GAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTT 636
              ||       |||||     |  || | || |   |  |       |  |||  | | |
Db        618 GAACTGAAAAAGATATCCGACTTAGGTGTTTGGCTAGTTGAGCTCGTATGGTCTTTTTGG 677

Qy        637 GCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGG 696
              || |||||||||| || || || || |  || |  || ||    ||  |     ||  |
Db        678 GCTTACATCTGGCTATACATAATCCTCGAGGTGTGGTCACCAAACGTAATTACACTTGTG 737

Qy        697 GAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGAT 756
              || |   |  | ||  |  |    |    | ||  | |  |||  || |  |    |||
Db        738 GAGGCATTATTGACAGTACTGCAATACGGATTGCTTCTAGTTCATGCGTACGCCCAAGAC 797

Qy        757 AAACGACTGCTCTTCT 772
              || |||  ||  | ||
Db        798 AAGCGATGGCCTTACT 813
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RESULT 3
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-F1s
US-08-232-463-14

  Query Match             2.8%;  Score 51.6;  DB 1;  Length 7218;
  Best Local Similarity   5.9%;  Pred. No. 3.7e-05;
  Matches   24;  Conservative  215;  Mismatches  169;  Indels    0;  Gaps    0;

Qy        395 CTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTT 454
              :: :::::  :::  ::::: :. ::::   ::::::: :::::    : ::::::::::
```

```
Db       1078 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1137

Qy        455 TAATTGAGGTGTGTGGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAG 514
              :  ::    : : :  :: :   ::: :: ::  :  :::    :::::: :: :: :
Db       1138 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1197

Qy        515 GGAGTGCAGCCTTCAACATGTTCATCATCATTGGCATCTGTGTCTACGTGATCCCAGACG 574
                  : :  :::::  : : ::: :: :: ::  : ::: : ::: : :  ::::   :
Db       1198 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1257

Qy        575 GAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCT 634
                    ::: :    ::   : ::: :   :::::::: :: :: :: :::    : :::
Db       1258 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1317

Qy        635 TTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTT 694
              :: ::: : :::  :::: : :  ::::  :  :::::::::::  : :  :::   :::
Db       1318 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1377

Qy        695 GGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAG 754
                    ::::::: ::::::::::::::::  : : : :::::::  :::   :
Db       1378 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYGTA 1437

Qy        755 ATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAG 802
                |||    |     |||  || ||| |||| | | ||      ||||
Db       1438 CCAAATTCTTCTATCTCTTTAACTACTTGCATAGATAGGTAATTACAG 1485
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RESULT 4
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
```

; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
US-08-232-463-14

Query Match 2.7%; Score 51; DB 1; Length 7218;
Best Local Similarity 3.4%; Pred. No. 5.8e-05;
Matches 9; Conservative 161; Mismatches 91; Indels 0; Gaps 0;

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Qy       1603 GAATGTGATACTATTCATGTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGG 1662
              |||| || ||| :   : :  :: ::::: :  :: :  : :::::  ::::    : ::
Db       1445 GAATTTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1386

Qy       1663 ACATCAGGTGCCCGGGGTACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAG 1722
              : :  ::: :   :::: : ::  :  :        :::: :: :::::::: ::  :::
Db       1385 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1326

Qy       1723 GGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACT 1782
              :: :: :: :::::    ::::: : : : :::::: .::::   ::::: :: ::::
Db       1325 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1266

Qy       1783 GTATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGAT 1842
              : : : :: ::: ::::::  ::  : :::::::::::::  :::::::: :: :::::
Db       1265 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1206

Qy       1843 GGGAAAGCCAGTATTGGGTGA 1863
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Db       1205 RRRRRRRRRRRRRRRRRRRR 1185
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RESULT 5
US-09-701-068-4
; Sequence 4, Application US/09701068
; Patent No. 6677506
; GENERAL INFORMATION:
; APPLICANT: Galil, Gad et al.
; TITLE OF INVENTION: DNA CODING FOR A Mg2+/H+ OR Zn2+/H+ EXCHANGER AND
TRANSGENIC PLANTS
; TITLE OF INVENTION: EXPRESSING SAME
; FILE REFERENCE: 01/21317
; CURRENT APPLICATION NUMBER: US/09/701,068
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 17

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;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 2803
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-701-068-4

  Query Match             2.4%;  Score 44.8;  DB 4;  Length 2803;
  Best Local Similarity   52.1%;  Pred. No. 0.0028;
  Matches  100;  Conservative    0;  Mismatches   92;  Indels    0;  Gaps    0;

Qy        477 GTTCATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTT 536
              |||   |  |   | ||| || |||   ||  |||| ||    || || ||  |  | ||
Db        950 GTTTTGTCATATAGGTCTTGGTCCTGGAACACTTGTTGGCTCAGCTGCATTTGATCTTTT 1009

Qy        537 CATCATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCA 596
              |  ||||   |   | ||||||   |||     ||  |||||       |||||    |
Db       1010 CCCCATCCACGCTGTTTGTGTCGTTGTGCCAAAAGCTGGAGAACTGAAAAAGATATCCGA 1069

Qy        597 TCTACGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATAT 656
                || | || |   |  |       |  |||  | | |  || ||||||||||| || ||
Db       1070 CTTAGGTGTTTGGCTAGTTGAGCTCGTATGGTCTTTTTGGGCTTACATCTGGCTATACAT 1129

Qy        657 GATTCTGGCAGT 668
              || || |  ||
Db       1130 AATCCTCGAGGT 1141


RESULT 6
US-08-182-175A-44
; Sequence 44, Application US/08182175A
; Patent No. 5559223
;  GENERAL INFORMATION:
;    APPLICANT:  Saverio Carl Falco
;    APPLICANT:  Sharon J. Keeler
;    APPLICANT:  Janet A. Rice
;    TITLE OF INVENTION:  Synthetic Storage Proteins with Defined Structure
Containing Pro
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  E.I. du Pont de Nemours and Company
;      STREET:  1007 Market Street
;      CITY:  Wilmington
;      STATE:  Delaware
;      COUNTRY:  USA
;      ZIP:  19898
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  Macintosh System, 6.0
;      SOFTWARE:  Microsoft Word, 4.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/182,175A
;      FILING DATE:
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/743,006
```

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;       FILING DATE:  9 August 1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Linda Axamethy Floyd
;       REGISTRATION NUMBER:  33,692
;       REFERENCE/DOCKET NUMBER:  BB-1031
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (302) 992-4929
;       TELEFAX:  (302) 892-7949
;       TELEX:  835420
;   INFORMATION FOR SEQ ID NO:  44:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  160 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     ORIGINAL SOURCE:
;       STRAIN:  E. coli
;       CELL TYPE:  DH5 alpha
;     IMMEDIATE SOURCE:
;       CLONE:  82-4
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  2..151
;       OTHER INFORMATION:  /function= "synthetic storage protein
;       OTHER INFORMATION:  /product= "protein"
;       OTHER INFORMATION:  /gene= "ssp"
;       OTHER INFORMATION:  /standard_name= "7.7.7.7.7.7.5"
US-08-182-175A-44

  Query Match              2.1%;  Score 38.4;  DB 1;  Length 160;
  Best Local Similarity   53.3%;  Pred. No. 0.042;
  Matches   81;  Conservative    0;  Mismatches   71;  Indels    0;  Gaps    0;

Qy       1708 GAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAATTC 1767
              | |||   |||  | || |  || |  ||   ||||| |      || ||    |||  |
Db          4 GGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGC 63

Qy       1768 AAGAATGATGAAACTGTATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAA 1827
              |    | ||| ||| | | ||  ||   ||||||||    |   || ||| ||   ||
Db         64 GATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAA 123

Qy       1828 GAGGATAGCAGAGATGGGAAAGCCAGTATTGG 1859
              |  ||| | ||||| |   ||| |   || ||
Db         124 GGCGATGGAAGAGAAGATGAAGGCGTGATAGG 155


RESULT 7
US-08-474-633A-53
; Sequence 53, Application US/08474633A
; Patent No. 5773691
;  GENERAL INFORMATION:
;    APPLICANT:  E. I. DU PONT DE NEMOURS AND
;    APPLICANT:  COMPANY
;    TITLE OF INVENTION:  CHIMERIC GENES AND
;    TITLE OF INVENTION:  METHODS FOR INCREASING
;    TITLE OF INVENTION:  INCREASING THE LYSINE
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;    TITLE OF INVENTION:  AND THREONINE CONTENT
;    TITLE OF INVENTION:  OF THE SEEDS OF PLANTS
;    NUMBER OF SEQUENCES:  107
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  E. I. DU PONT DE NEMOURS
;      ADDRESSEE:  AND COMPANY
;      STREET:  1007 MARKET STREET
;      CITY:  WILMINGTON
;      STATE:  DELAWARE
;      COUNTRY:  U.S.A.
;      ZIP:  19898
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  MICROSOFT WORD VERSION 2.0C
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,633A
;      FILING DATE:
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BARBARA C. SIEGELL
;      REGISTRATION NUMBER:  30,684
;      REFERENCE/DOCKET NUMBER:  BB-1037-C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  302-992-4931
;      TELEFAX:  302-773-0164
;      TELEX:  835420
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  160 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;      STRAIN:  E. coli
;      CELL TYPE:  DH5 alpha
;    IMMEDIATE SOURCE:
;      CLONE:  82-4
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2..151
;      OTHER INFORMATION:  /function= "synthetic
;      OTHER INFORMATION:  storage protein
;      OTHER INFORMATION:  /product= "protein"
;      OTHER INFORMATION:  /gene= "ssp"
;      OTHER INFORMATION:  /standard_name=
;      OTHER INFORMATION:  "7.7.7.7.7.7.5"
US-08-474-633A-53

  Query Match              2.1%;  Score 38.4;  DB 1;  Length 160;
  Best Local Similarity   53.3%;  Pred. No. 0.042;
  Matches   81;  Conservative    0;  Mismatches   71;  Indels    0;  Gaps    0;

Qy       1708 GAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAATTC 1767
              | |||   |||  | || |  || |  ||   ||||| |      || ||    |||  |
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Db          4 GGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGC 63

Qy       1768 AAGAATGATGAAACTGTATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAA 1827
              |    | ||| ||| | | ||  ||   ||||||||    |   || ||| ||   ||
Db         64 GATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAA 123

Qy       1828 GAGGATAGCAGAGATGGGAAAGCCAGTATTGG 1859
              |  ||| | ||||| |   ||| |   || ||
Db        124 GGCGATGGAAGAGAAGATGAAGGCGTGATAGG 155


RESULT 8
US-08-823-771-53
; Sequence 53, Application US/08823771
; Patent No. 6459019
;   GENERAL INFORMATION:
;        APPLICANT: E. I. DU PONT DE NEMOURS AND
;                   COMPANY
;        TITLE OF INVENTION: CHIMERIC GENES AND
;                            METHODS FOR INCREASING
;                            INCREASING THE LYSINE
;                            AND THREONINE CONTENT
;        NUMBER OF SEQUENCES: 107
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: E. I. DU PONT DE NEMOURS
;                        AND COMPANY
;             STREET: 1007 MARKET STREET
;             CITY: WILMINGTON
;             STATE: DELAWARE
;             COUNTRY: U.S.A.
;             ZIP: 19898
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: FLOPPY DISK
;             COMPUTER: IBM PC COMPATIBLE
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: MICROSOFT WORD VERSION 2.0C
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/823,771
;             FILING DATE: 24-Mar-1997
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/474,633
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BARBARA C. SIEGELL
;             REGISTRATION NUMBER: 30,684
;             REFERENCE/DOCKET NUMBER: BB-1037-C
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 302-992-4931
;             TELEFAX: 302-773-0164
;             TELEX: 835420
;   INFORMATION FOR SEQ ID NO: 53:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 160 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
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;         MOLECULE TYPE: DNA (genomic)
;         ORIGINAL SOURCE:
;              STRAIN: E. coli
;              CELL TYPE: DH5 alpha
;         IMMEDIATE SOURCE:
;              CLONE: 82-4
;         FEATURE:
;              NAME/KEY:   CDS
;              LOCATION:   2..151
;              OTHER INFORMATION:   /function= "synthetic
;              storage protein
;              /product= "protein"
;              /gene= "ssp"
;              /standard_name=
;              "7.7.7.7.7.7.5"
;         SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-08-823-771-53

  Query Match              2.1%;  Score 38.4;  DB 4;  Length 160;
  Best Local Similarity   53.3%;  Pred. No. 0.042;
  Matches   81;  Conservative    0;  Mismatches   71;  Indels    0;  Gaps    0;

Qy       1708 GAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAATTC 1767
              | |||   |||  | || |  || |  ||   ||||| |      || ||    |||  |
Db          4 GGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGC 63

Qy       1768 AAGAATGATGAAACTGTATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAA 1827
               |    | ||| ||| | | ||  ||   ||||||||    |   || ||| ||   ||
Db         64 GATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAA 123

Qy       1828 GAGGATAGCAGAGATGGGAAAGCCAGTATTGG 1859
              |  ||| | ||||| |   ||| |   || ||
Db         124 GGCGATGGAAGAGAAGATGAAGGCGTGATAGG 155


RESULT 9
PCT-US92-06412-44
; Sequence 44, Application PC/TUS9206412
;  GENERAL INFORMATION:
;    APPLICANT:  Saverio Carl Falco
;    APPLICANT:  Sharon J. Keeler
;    APPLICANT:  Janet A. Rice
;    TITLE OF INVENTION:  Synthetic Storage Proteins with Defined Structure
Containing Pro
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  E.I. du Pont de Nemours and Company
;      STREET:  1007 Market Street
;      CITY:  Wilmington
;      STATE:  Delaware
;      COUNTRY:  USA
;      ZIP:  19898
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  Macintosh System, 6.0
;      SOFTWARE:  Microsoft Word, 4.0
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/06412
;      FILING DATE:  19920807
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/743,006
;      FILING DATE:  9 August 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Linda Axamethy Floyd
;      REGISTRATION NUMBER:  33,692
;      REFERENCE/DOCKET NUMBER:  BB-1031
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (302) 992-4929
;      TELEFAX:  (302) 892-7949
;      TELEX:  835420
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  160 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;      STRAIN:  E. coli
;      CELL TYPE:  DH5 alpha
;    IMMEDIATE SOURCE:
;      CLONE:  82-4
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  2..151
;      OTHER INFORMATION:  /function= "synthetic storage protein
;      OTHER INFORMATION:  /product= "protein"
;      OTHER INFORMATION:  /gene= "ssp"
;      OTHER INFORMATION:  /standard_name= "7.7.7.7.7.7.5"
PCT-US92-06412-44

  Query Match              2.1%;  Score 38.4;  DB 5;  Length 160;
  Best Local Similarity   53.3%;  Pred. No. 0.042;
  Matches   81;  Conservative    0;  Mismatches   71;  Indels    0;  Gaps    0;

Qy       1708 GAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAATTC 1767
              | |||   |||  | || |  || |  ||   ||||| |      || ||    |||  |
Db          4 GGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGC 63

Qy       1768 AAGAATGATGAAACTGTATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCCAA 1827
               |    |  ||| ||| | | ||  ||   ||||||||    |   || ||| ||   ||
Db         64 GATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAAGGCGATGGAGGAGAAGCTGAA 123

Qy       1828 GAGGATAGCAGAGATGGGAAAGCCAGTATTGG 1859
              |  ||| | ||||| |   ||| |   || ||
Db        124 GGCGATGGAAGAGAAGATGAAGGCGTGATAGG 155


RESULT 10
US-09-310-463-3/c
; Sequence 3, Application US/09310463A
; Patent No. 6384203
```

; GENERAL INFORMATION:
; APPLICANT: Cosman, David J.
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Borges, Luis
; TITLE OF INVENTION: Family of Immunoregulators Designated Leukocyte
Immunoglobulin-
; TITLE OF INVENTION: Like Receptors (LIR)
; FILE REFERENCE: 2624-A
; CURRENT APPLICATION NUMBER: US/09/310,463A
; CURRENT FILING DATE: 1999-05-12
; EARLIER APPLICATION NUMBER: 08/842,248
; EARLIER FILING DATE: 1997-04-24
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2777
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (168)..(2126)
US-09-310-463-3

Query Match 2.1%; Score 38.4; DB 3; Length 2777;
Best Local Similarity 49.0%; Pred. No. 0.31;
Matches 102; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

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Db        280 ACAGAGCCTGGTTCAGCCCAGAGGGTGGGCTTGGGGAGGTGCCCTGCCTGCACGTGGGTC 221

Qy       1363 CTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTT 1422
              |||  |||  ||   | || ||   || ||      |  |  || |  | |      | |
Db        220 CTGGGGCCCAGACTCAGCCCGAGACAGATCAGGACCGTGAGGATGGGGGTCATGGCGTCT 161

Qy       1423 GAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCA 1482
                    ||  |   ||| || | || |||||  |    |||| |  |  |  |  |||
Db        160 CCTCCCACTGCCCTGCTCTGTGGATGGATGAGCCCTCGGTGCATGGCAGTCGTCCCTCCA 101

Qy       1483 GAGGAGGGGATGCCTCCAGCAATATTCA 1510
              |    || ||||| ||  | || |  ||
Db        100 GCCCTGGAGATGCTTCAGGGAAGACCCA 73
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RESULT 11
US-08-842-248A-3/c
; Sequence 3, Application US/08842248A
; Patent No. 6448035
; GENERAL INFORMATION:
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Family of Immunoregulators Designated
; TITLE OF INVENTION: Leukocyte Immunoglobulin-Like Receptors (LIR)
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle

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;       STATE:  WA
;       COUNTRY:  US
;       ZIP:  98101
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM/PC Compatible
;       OPERATING SYSTEM:  Microsoft Word 7.0
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/842,248A
;       FILING DATE:  April 24, 1997
;       CLASSIFICATION:  536
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Henry, Janis C.
;       REGISTRATION NUMBER:  34,347
;       REFERENCE/DOCKET NUMBER:  2624
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (206) 587-0430
;       TELEFAX:  (206) 233-0644
;       TELEX:  756822
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2777 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     IMMEDIATE SOURCE:
;       LIBRARY:  18a3
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  168..2123
US-08-842-248A-3

  Query Match             2.1%;  Score 38.4;  DB 4;  Length 2777;
  Best Local Similarity   49.0%;  Pred. No. 0.31;
  Matches  102;  Conservative    0;  Mismatches  106;  Indels    0;  Gaps    0;

Qy       1303 ACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTT 1362
              ||||||  ||||||  |||  |    | ||          || | | |   |||||  |||
Db        280 ACAGAGCCTGGTTCAGCCCAGAGGGTGGGCTTGGGGAGGTGCCCTGCCTGCACGTGGGTC 221

Qy       1363 CTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTT 1422
              |||  |||  ||   | || ||   || ||      |  |  || |  | |      | |
Db        220 CTGGGGCCCAGACTCAGCCCGAGACAGATCAGGACCGTGAGGATGGGGGTCATGGCGTCT 161

Qy       1423 GAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCA 1482
                    ||  |   ||| || | || |||||  |    |||| |  |  |  |  |||
Db        160 CCTCCCACTGCCCTGCTCTGTGGATGGATGAGCCCTCGGTGCATGGCAGTCGTCCCTCCA 101

Qy       1483 GAGGAGGGGATGCCTCCAGCAATATTCA 1510
              |    || ||||| ||  | || |  ||
Db        100 GCCCTGGAGATGCTTCAGGGAAGACCCA 73


RESULT 12
US-09-007-005-17/c
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; Sequence 17, Application US/09007005B
; Patent No. 6258558
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350003
; CURRENT APPLICATION NUMBER: US/09/007,005B
; CURRENT FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 289
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-007-005-17

Query Match 2.0%; Score 37.4; DB 3; Length 289;
Best Local Similarity 6.5%; Pred. No. 0.13;
Matches 14; Conservative 93; Mismatches 108; Indels 0; Gaps 0;

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Qy        608 TCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAG 667
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Db        225 YCYTYGYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYN 166

Qy        668 TCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAG 727
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Db        165 YSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYN 106

Qy        728 TGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACA 787
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Db        105 YSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYCYAYTYTYGYT 46

Qy        788 AAAAGTACCGCACAGACAAACACCGAGGAATTATC 822
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Db         45 YAYAYTYTYGYTYAYAYAYTYAYGYTYAYAYTYTY 11
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RESULT 13
US-09-244-796-17/c
; Sequence 17, Application US/09244796
; Patent No. 6281344
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.

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;  APPLICANT: Liu, Rihe
;  TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
;  TITLE OF INVENTION: FUSIONS
;  FILE REFERENCE: 00786/350007
;  CURRENT APPLICATION NUMBER: US/09/244,796
;  CURRENT FILING DATE: 1999-02-05
;  EARLIER APPLICATION NUMBER: 60/035,963
;  EARLIER FILING DATE: 1997-01-27
;  EARLIER APPLICATION NUMBER: 60/064,491
;  EARLIER FILING DATE: 1997-11-06
;  EARLIER APPLICATION NUMBER: 09/007,005
;  EARLIER FILING DATE: 1998-01-14
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 289
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Translation template
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(289)
;   OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17

  Query Match              2.0%;  Score 37.4;  DB 3;  Length 289;
  Best Local Similarity   6.5%;  Pred. No. 0.13;
  Matches   14;  Conservative   93;  Mismatches  108;  Indels    0;  Gaps    0;

Qy        608 TCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAG 667
              :|:|: ::  : :   :  :  : ::: : ::: : :::   ::: : ::  : ::
Db        225 YCYTYGYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYN 166

Qy        668 TCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAG 727
              ::: : ::: :       :::   : :       : ::: : : : : ::: : : :
Db        165 YSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYN 106

Qy        728 TGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACA 787
              ::: : ::: : ::  :  :    :   :   :   ::: : ::: :   :|: : : :
Db        105 YSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYCYAYTYTYGYT 46

Qy        788 AAAAGTACCGCACAGACAAACACCGAGGAATTATC 822
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Db         45 YAYAYTYTYGYTYAYAYAYTYAYGYTYAYAYTYTY 11


RESULT 14
US-09-148-545-110/c
; Sequence 110, Application US/09148545
; Patent No. 6590075
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 70 Human Secreted Proteins
;  FILE REFERENCE: PZ001P1
;  CURRENT APPLICATION NUMBER: US/09/148,545
;  CURRENT FILING DATE: 1998-09-04
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; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,161
; EARLIER FILING DATE: 1997-03-07
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; EARLIER FILING DATE: 1997-03-07
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; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
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; EARLIER APPLICATION NUMBER: 60/047,612

; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,601
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; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
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; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,893
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22

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; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 05-Sep-1997
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
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; EARLIER APPLICATION NUMBER: 60/047,594
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; EARLIER APPLICATION NUMBER: 60/047,589
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
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; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
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; EARLIER APPLICATION NUMBER: 60/056,881

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;  EARLIER APPLICATION NUMBER: 60/056,909
;  EARLIER FILING DATE: 1997-08-22
;  EARLIER APPLICATION NUMBER: 60/056,875
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;  EARLIER FILING DATE: 1997-08-22
;  EARLIER APPLICATION NUMBER: 60/056,908
;  EARLIER FILING DATE: 1997-08-22
;  EARLIER APPLICATION NUMBER: 60/048,964
;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/057,650
;  EARLIER FILING DATE: 1997-09-05
;  EARLIER APPLICATION NUMBER: 60/056,884
;  EARLIER FILING DATE: 1997-08-22
;  NUMBER OF SEQ ID NOS: 280
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 110
;   LENGTH: 1320

  Query Match              2.0%;  Score 37.2;  DB 4;  Length 1320;
  Best Local Similarity   47.7%;  Pred. No. 0.44;
  Matches  105;  Conservative    1;  Mismatches  114;  Indels    0;  Gaps    0;

Qy        554 GTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCA 613
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Db        810 GTGTCACCGTCATCCCAGCCACGGCTGCTCGCCCCAGGTGACAGTGTGGCAGCTGAAGTC 751

Qy        614 TCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCT 673
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Db        750 TCCCGGCTGCCAGGGCTCACTTCCAAGCTTACAGAACTCGTGTCACTCATTGTGTCAGCT 691

Qy        674 CCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTG 733
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Db        690 CCTGTGCCATCCACCTGGGTGTCAATGGCCTCCACAAGCCCCCGCCATTTCCACTCTGTC 631

Qy        734 TCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTA 773
              ||||||    | ||     |||       |||| :| | |
Db        630 TCCTTCATCTCAGGCACATAGAAGTCTCCCTGCCSTGCCA 591


RESULT 15
US-09-270-767-31616
; Sequence 31616, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31616
;   LENGTH: 740
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; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-31616

Query Match 2.0%; Score 37; DB 4; Length 740;
Best Local Similarity 47.6%; Pred. No. 0.34;
Matches 109; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

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Db         18 AGGACATCGAGGGCAACTGGCACCAGAAACATCCCGTTGTGATGCAGTGCTTCCAGGAGT 77

Qy        908 CCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATC 967
               |  | |   | |  | |     ||||    ||  |||  |   ||    | ||  ||
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Qy        968 TGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATG 1027
              | | | |||       |||   ||   |||||    || |||| |||   | ||| | |
Db        138 AGTACCGAAATGTGGTCGAGGGCGAGGAAGATCCCACGGAGGAGTTGGTGGAATACGAGG 197

Qy       1028 CTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCAC 1076
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Db        198 TCGACGACCCTAAGCAGAAGAAGTGGGACTGCGAGTCTATCCTGTCCAC 246
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Search completed: January 22, 2005, 17:35:38
Job time : 154.533 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 22, 2005, 07:25:49 ; Search time 985.631 Seconds
(without alignments)
10860.644 Million cell updates/sec

Title: US-10-054-680-3
Perfect score: 1863
Sequence: 1 atggcgtggttaaggttgca.....ggaaagccagtattgggtga 1863

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
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21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1863	100.0	1863	13	US-10-054-680-3	Sequence 3, Appli
2	1784.6	95.8	2766	13	US-10-054-680-1	Sequence 1, Appli
3	1784.6	95.8	3812	13	US-10-054-680-5	Sequence 5, Appli
4	1784.4	95.8	2534	15	US-10-256-537-1	Sequence 1, Appli
5	1784.4	95.8	2534	15	US-10-256-537-3	Sequence 3, Appli
6	1783	95.7	2781	14	US-10-275-116-1	Sequence 1, Appli
7	1783	95.7	2782	9	US-09-804-474A-1	Sequence 1, Appli
8	1782.8	95.7	126512	9	US-09-804-474A-3	Sequence 3, Appli
9	1782.4	95.7	2813	15	US-10-114-153-1	Sequence 1, Appli
10	1782.4	95.7	2840	15	US-10-114-153-3	Sequence 3, Appli
11	1694.8	91.0	2685	15	US-10-114-153-5	Sequence 5, Appli
12	821.4	44.1	823	15	US-10-029-386-20265	Sequence 20265, A
13	810.6	43.5	4087	9	US-09-901-419-1	Sequence 1, Appli
14	785.2	42.1	1836	9	US-09-864-761-16939	Sequence 16939, A
15	784.8	42.1	5438	18	US-10-357-930-24294	Sequence 24294, A
16	783.2	42.0	6106	16	US-10-062-674-1648	Sequence 1648, Ap
17	713.4	38.3	3004	16	US-10-388-934-506	Sequence 506, App
18	692.4	37.2	4282	14	US-10-281-866-1	Sequence 1, Appli
19	692.4	37.2	4282	14	US-10-281-866-3	Sequence 3, Appli
20	503.4	27.0	505	15	US-10-029-386-6536	Sequence 6536, Ap
21	494	26.5	551	15	US-10-029-386-4103	Sequence 4103, Ap
22	366	19.6	366	15	US-10-029-386-17804	Sequence 17804, A
23	334.4	17.9	507	15	US-10-029-386-4003	Sequence 4003, Ap
24	180	9.7	180	15	US-10-029-386-17706	Sequence 17706, A
25	164.2	8.8	459	9	US-09-864-761-102	Sequence 102, App
26	146.6	7.9	1132	15	US-10-369-493-30006	Sequence 30006, A
27	91.4	4.9	1792	15	US-10-369-493-29835	Sequence 29835, A
28	79	4.2	477	10	US-09-918-995-2005	Sequence 2005, Ap
29	79	4.2	1187	15	US-10-243-552-809	Sequence 809, App
c 30	79	4.2	2859	18	US-10-723-860-7370	Sequence 7370, Ap
31	77.4	4.2	1248	18	US-10-425-115-125495	Sequence 125495,
32	71.6	3.8	1617	9	US-09-938-842A-2591	Sequence 2591, Ap
33	71.6	3.8	1617	11	US-09-938-842A-2591	Sequence 2591, Ap
34	58.2	3.1	862	16	US-10-424-599-86000	Sequence 86000, A
c 35	57.4	3.1	173	18	US-10-674-124A-2603	Sequence 2603, Ap
36	45.2	2.4	1487	17	US-10-437-963-77130	Sequence 77130, A
37	41.2	2.2	55005	18	US-10-719-993-6968	Sequence 6968, Ap
c 38	41.2	2.2	318760	18	US-10-719-993-6765	Sequence 6765, Ap
39	39.6	2.1	1635	16	US-10-282-122A-29169	Sequence 29169, A
40	39.6	2.1	30306	13	US-10-087-192-523	Sequence 523, App
c 41	39	2.1	77922	17	US-10-741-601-5674	Sequence 5674, Ap
42	39	2.1	203127	17	US-10-741-601-5654	Sequence 5654, Ap
43	38.8	2.1	244	18	US-10-674-124A-612	Sequence 612, App
44	38.8	2.1	2318	17	US-10-437-963-21282	Sequence 21282, A
45	38.8	2.1	2967	17	US-10-437-963-21285	Sequence 21285, A

ALIGNMENTS

RESULT 1
US-10-054-680-3
; Sequence 3, Application US/10054680

; Publication No. US20020132998A1
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. US20020132998A1el Human Ion Exchanger Proteins and Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0301-USA
; CURRENT APPLICATION NUMBER: US/10/054,680
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/263,384
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1863
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-054-680-3

Query Match 100.0%; Score 1863; DB 13; Length 1863;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1863; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Db        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Db        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Db        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
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Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
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Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
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Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
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Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
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Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
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Qy       1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGG 1860
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Db       1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGATGGGAAAGCCAGTATTGGG 1860

Qy       1861 TGA 1863
              |||
Db       1861 TGA 1863
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RESULT 2
US-10-054-680-1
; Sequence 1, Application US/10054680
; Publication No. US20020132998A1
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. US20020132998A1el Human Ion Exchanger Proteins and Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0301-USA
; CURRENT APPLICATION NUMBER: US/10/054,680
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/263,384
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1

; LENGTH: 2766
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-054-680-1

Query Match 95.8%; Score 1784.6; DB 13; Length 2766;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
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Db         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
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Db        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
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Db        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
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Db        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
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Db        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
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Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
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Db        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
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Db        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
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Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Db        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
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Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
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Db        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
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Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
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Db        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
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Db       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
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Db       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620

Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
                ||||||||||||||||||||||||||||||||||||    |||||  |  ||  |
Db       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1796

Qy       1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
                | | |  || | ||| |||||||   |    |    |||||
Db       1797 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837
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RESULT 3
US-10-054-680-5
; Sequence 5, Application US/10054680
; Publication No. US20020132998A1
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. US20020132998A1el Human Ion Exchanger Proteins and Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0301-USA
; CURRENT APPLICATION NUMBER: US/10/054,680
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/263,384
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3812
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-054-680-5

Query Match 95.8%; Score 1784.6; DB 13; Length 3812;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1813; Conservative 0; Mismatches 24; Indels 4; Gaps 1;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        618 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 677

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 737

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        738 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 797

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        798 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 857

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        858 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 917

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        918 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 977

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        978 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 1037

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1038 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 1097

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1098 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 1157

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1158 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 1217

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1218 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1277

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1278 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1337

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1338 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1397

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1398 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 1457

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1458 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 1517

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1518 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1577

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1578 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1637
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Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1638 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1697

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1698 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1757

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1758 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1817

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1818 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1877

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1878 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1937

Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1938 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1997

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1998 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 2057

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2058 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 2117

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2118 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 2177

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2178 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 2237

Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2238 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 2297

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2298 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2357

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
             |||||||||||||||||||||||||||||||||||||||    |||||  |  ||  |
Db       2358 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 2413

Qy       1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
             | | |  || | ||| |||||||   |    |    |||||
Db       2414 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 2454
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RESULT 4
US-10-256-537-1
; Sequence 1, Application US/10256537
; Publication No. US20030162196A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: METHODS OF USING 69039, A NOVEL HUMAN
; TITLE OF INVENTION: NA/CA EXCHANGER FAMILY MEMBER
; FILE REFERENCE: MPI01-231P1RM
; CURRENT APPLICATION NUMBER: US/10/256,537
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/325,737
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2534
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-256-537-1

Query Match 95.8%; Score 1784.4; DB 15; Length 2534;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 402

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 462

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 522

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 582

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        583 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 642

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 702

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        703 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 762

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        763 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 822
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Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        823 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 882

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        883 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 942

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        943 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1002

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1003 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1062

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1122

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1123 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 1182

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1183 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 1242

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1243 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1302

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1303 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1362

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1363 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1422

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1423 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1482

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1483 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1542

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1543 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1602

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1603 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1662
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Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1663 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1722

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1723 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1782

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1783 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1842

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1843 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1902

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1903 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1962

Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1963 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 2022

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2023 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2082

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
             |||||||||||||||||||||||||||||||||||||||||||||| |
Db       2083 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGT 2128
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RESULT 5
US-10-256-537-3
; Sequence 3, Application US/10256537
; Publication No. US20030162196A1
; GENERAL INFORMATION:
;  APPLICANT: Carroll, Joseph M.
;  TITLE OF INVENTION: METHODS OF USING 69039, A NOVEL HUMAN
;  TITLE OF INVENTION:  NA/CA EXCHANGER FAMILY MEMBER
;  FILE REFERENCE: MPI01-231P1RM
;  CURRENT APPLICATION NUMBER: US/10/256,537
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: 60/325,737
;  PRIOR FILING DATE: 2001-09-28
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 2534
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (343)...(2130)
US-10-256-537-3
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Query Match 95.8%; Score 1784.4; DB 15; Length 2534;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1785; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 402

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 462

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 522

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 582

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        583 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 642

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        643 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 702

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        703 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 762

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        763 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 822

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        823 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 882

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        883 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 942

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        943 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 1002

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1003 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 1062

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1063 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 1122

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
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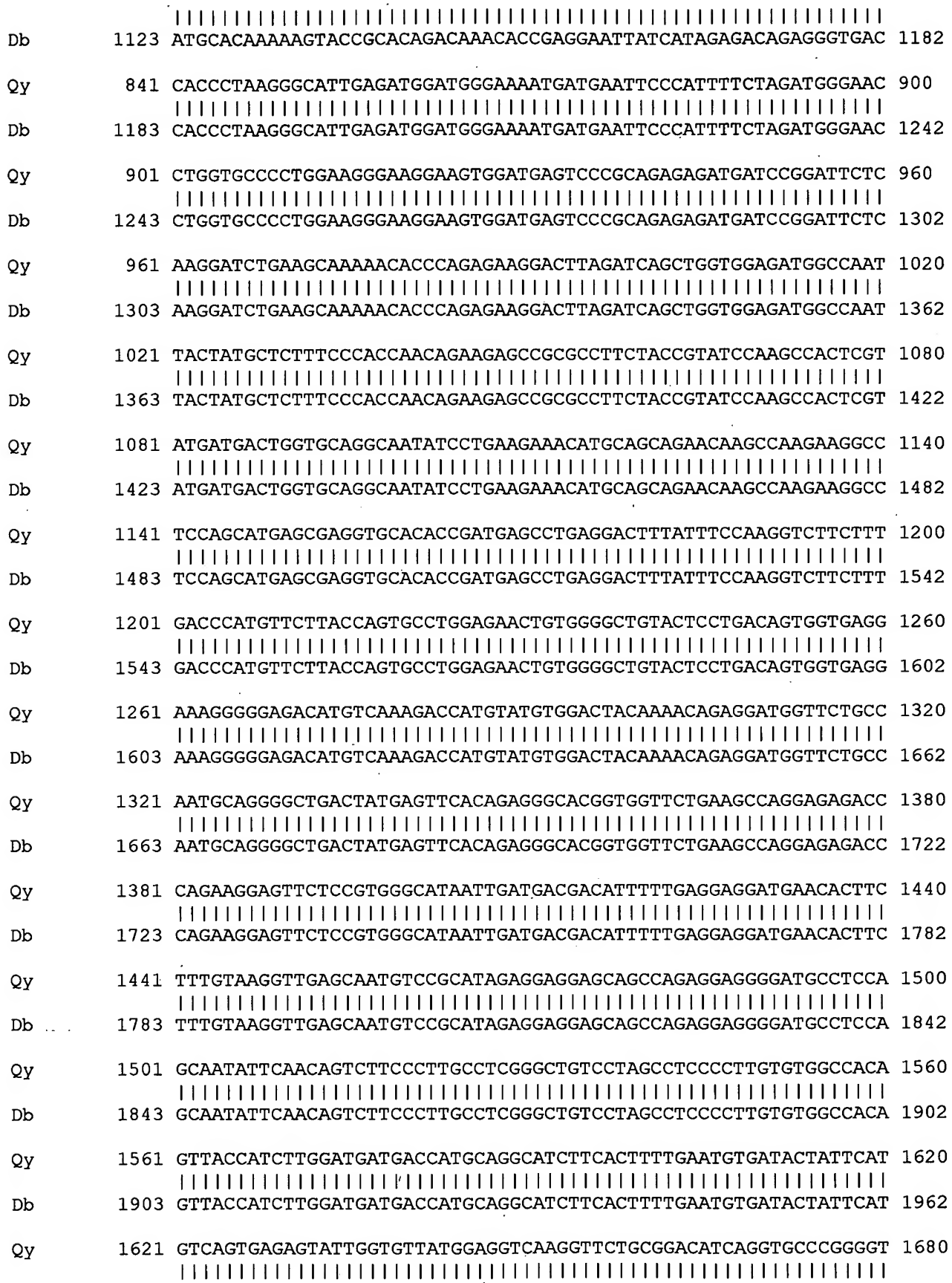

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Db       1963 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 2022

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2023 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 2082

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
              |||||||||||||||||||||||||||||||||||||||||||| |
Db       2083 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGT 2128


RESULT 6
US-10-275-116-1
; Sequence 1, Application US/10275116
; Publication No. US20030096312A1
; GENERAL INFORMATION:
;  APPLICANT: Merck Patent GmbH
;  TITLE OF INVENTION: No. US20030096312A1el natrium-calium exchanger protein
;  FILE REFERENCE: HNCX3CWWS
;  CURRENT APPLICATION NUMBER: US/10/275,116
;  CURRENT FILING DATE:  2002-11-01
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 2781
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2781)
US-10-275-116-1

  Query Match             95.7%;  Score 1783;  DB 14;  Length 2781;
  Best Local Similarity   98.4%;  Pred. No. 0;
  Matches 1812;  Conservative    0;  Mismatches   25;  Indels    4;  Gaps    1;

Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ..|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
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Db        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
                                                                                
Db        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
                                                                                
Db        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
                                                                                
Db        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
                                                                                
Db        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
                                                                                
Db        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
                                                                                
Db        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
                                                                                
Db        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
                                                                                
Db        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
                                                                                
Db        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
                                                                                
Db        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
                                                                                
Db        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT. 1020

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
                                                                                
Db       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGTGCCTTCTACCGTATCCAAGCCACTCGT 1080

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
                                                                                
Db       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
                                                                                
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Db       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320

Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620

Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
             ||||||||||||||||||||||||||||||||||||    ||||| |  ||  |
Db       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1796

Qy       1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
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Db       1797 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1837
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RESULT 7
US-09-804-474A-1
; Sequence 1, Application US/09804474A
; Patent No. US20020119518A1
; GENERAL INFORMATION:
; APPLICANT: KODET, Stefan et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF

```
;  FILE REFERENCE: CL000891
;  CURRENT APPLICATION NUMBER: US/09/804,474A
;  CURRENT FILING DATE:  2001-03-13
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 2782
;   TYPE: DNA
;   ORGANISM: Human
US-09-804-474A-1

  Query Match             95.7%;  Score 1783;  DB 9;  Length 2782;
  Best Local Similarity   98.4%;  Pred. No. 0;
  Matches 1812;  Conservative    0;  Mismatches   25;  Indels    4;  Gaps    1;

Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 69

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 129

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 189

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 249

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 309

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 369

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 429

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 489

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 549

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 609

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        610 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 669

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 729

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 789

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 849

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 909

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        910 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATCCTC 969

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1029

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1030 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1089

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1090 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1149

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
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Db       1150 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1209

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1210 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1269

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1270 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1329

Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1330 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1389

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1390 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1449

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1450 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1509
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Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1510 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1569

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1570 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1629

Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1630 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1689

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1690 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1749

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTATGTGACAGACAGGAA 1800
             ||||||||||||||||||||||||||||||||||||||||    |||||  |  ||  |
Db       1750 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAAC----TGTGAAAACCATAAG 1805

Qy       1801 GCTGACTATGGAAGAAGAGGAGGCCAAGAGGATAGCAGAGA 1841
             | | |  || | ||| |||||||   |    |    |||||
Db       1806 GGTTAAAATAGTAGATGAGGAGGAATACGAAAGGCAAGAGA 1846
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RESULT 8
US-09-804-474A-3
; Sequence 3, Application US/09804474A
; Patent No. US20020119518A1
; GENERAL INFORMATION:
; APPLICANT: KODET, Stefan et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000891
; CURRENT APPLICATION NUMBER: US/09/804,474A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 126512
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(126512)
;   OTHER INFORMATION: n = A,T,C or G
US-09-804-474A-3

  Query Match   95.7%; Score 1782.8; DB 9; Length 126512;
  Best Local Similarity   99.9%; Pred. No. 0;
  Matches 1784; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db       2010 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 2069

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2070 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 2129

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2130 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 2189

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2190 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 2249

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2250 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 2309

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2310 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 2369

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db       2370 ACCAGCACAACAACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 2429

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2430 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 2489

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2490 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 2549

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2550 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 2609

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2610 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 2669

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2670 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 2729

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2730 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 2789

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2790 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 2849

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2850 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 2909
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Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2910 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 2969

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2970 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 3029

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3030 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 3089

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3090 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 3149

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3150 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 3209

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3210 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 3269

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3270 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 3329

Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3330 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 3389

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3390 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 3449

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3450 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 3509

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3510 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 3569

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3570 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 3629

Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3630 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 3689

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3690 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 3749
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Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTAT 1786
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Db       3750 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGTGT 3795


RESULT 9
US-10-114-153-1
; Sequence 1, Application US/10114153
; Publication No. US20030185815A1
; GENERAL INFORMATION:
;  APPLICANT: Padigaru, Muralidhara
;  APPLICANT:  Shenoy, Suresh
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Mezes, Peter
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Guo, Xiaojia
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Casman, Stacie
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Li, Li
;  APPLICANT:  Zerhusen, Bryan
;  APPLICANT:  Tchernev, Velizar
;  APPLICANT:  Gangolli, Esha
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Spytek, Kimberly
;  APPLICANT:  Malyankar, Uriel
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Miller, Charles
;  APPLICANT:  Taupier, Raymond J. Jr.
;  APPLICANT:  Heyes, Melvyn
;  APPLICANT:  Ju, Jingfang
;  APPLICANT:  Peyman, John
;  APPLICANT:  Catterton, Elina
;  APPLICANT:  MacDougall, John
;  APPLICANT:  Edinger, Shlomit
;  APPLICANT:  Stone, David
;  APPLICANT:  Mazur, Ann
;  TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES,
NUCLEIC ACIDS
;  TITLE OF INVENTION:  ENCODING THE ANTIGENS, AND METHODS OF USE
;  FILE REFERENCE: 21402-322A
;  CURRENT APPLICATION NUMBER: US/10/114,153
;  CURRENT FILING DATE:  2002-08-06
;  PRIOR APPLICATION NUMBER: 60/281086
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282020
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: 60/282930
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283512
;  PRIOR FILING DATE: 2001-04-12
;  PRIOR APPLICATION NUMBER: 60/283444
;  PRIOR FILING DATE: 2001-04-12
;  PRIOR APPLICATION NUMBER: 60/283657
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; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 1
;   LENGTH: 2813
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (9)..(2793)
US-10-114-153-1

  Query Match   95.7%; Score 1782.4; DB 15; Length 2813;
  Best Local Similarity   99.9%; Pred. No. 0;
  Matches 1783; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
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Db          9 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 68

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 128

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 188

Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 248

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 308

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 368

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 428

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 488

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 548
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Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        549 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 608

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        609 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 668

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        669 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 728

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        729 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 788

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        789 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 848

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        849 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 908

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        909 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 968

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        969 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1028

Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       1029 TACTATGCTCTTTCCCACCAACAGAAGAGCCGTGCCTTCTACCGTATCCAAGCCACTCGT 1088

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1089 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1148

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1149 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1208

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1209 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1268

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1269 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1328

Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1329 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1388
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Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1389 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1448

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1449 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1508

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
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Db       1509 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1568

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
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Db       1569 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1628

Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
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Db       1629 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1688

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
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Db       1689 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1748

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGT 1784
             |||||||||||||||||||||||||||||||||||||||||||||
Db       1749 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGT 1792
```

RESULT 10
US-10-114-153-3
; Sequence 3, Application US/10114153
; Publication No. US20030185815A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John

; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 3
; LENGTH: 2840
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (63)..(2838)
US-10-114-153-3

Query Match 95.7%; Score 1782.4; DB 15; Length 2840;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1783; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 ATGGCGTGGTTAAGGTTGCAGCCTCTCACCTCTGCCTTCCTCCATTTTGGGCTGGTTACC 122

Qy         61 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 TTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGC 182

Qy        121 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 ACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTG 242
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Qy        181 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 CCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGGGTCATTGTCTAT 302

Qy        241 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 TTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGACCGCTTCATGGCA 362

Qy        301 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 TCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAGAAACCCAATGGAGAA 422

Qy        361 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        423 ACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAACCTGACCCTTATGGCC 482

Qy        421 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        483 CTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTC 542

Qy        481 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 ATTGCTGGTGATCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATC 602

Qy        541 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        603 ATCATTGGCATCTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTA 662

Qy        601 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        663 CGAGTCTTCTTCATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATT 722

Qy        661 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        723 CTGGCAGTCTTCTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTC 782

Qy        721 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        783 TTTCCAGTGTGTGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATAC 842

Qy        781 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        843 ATGCACAAAAAGTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGAC 902

Qy        841 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        903 CACCCTAAGGGCATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAAC 962

Qy        901 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        963 CTGGTGCCCCTGGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTC 1022

Qy        961 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1023 AAGGATCTGAAGCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAAT 1082
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Qy       1021 TACTATGCTCTTTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGT 1080
             |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1083 TACTATGCTCTTTCCCACCAACAGAAGAGCCGTGCCTTCTACCGTATCCAAGCCACTCGT 1142

Qy       1081 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1143 ATGATGACTGGTGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCC 1202

Qy       1141 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1203 TCCAGCATGAGCGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTT 1262

Qy       1201 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1263 GACCCATGTTCTTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGG 1322

Qy       1261 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1323 AAAGGGGGAGACATGTCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCC 1382

Qy       1321 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1383 AATGCAGGGGCTGACTATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACC 1442

Qy       1381 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1443 CAGAAGGAGTTCTCCGTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTC 1502

Qy       1441 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1503 TTTGTAAGGTTGAGCAATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCA 1562

Qy       1501 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1563 GCAATATTCAACAGTCTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACA 1622

Qy       1561 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1623 GTTACCATCTTGGATGATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCAT 1682

Qy       1621 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1683 GTCAGTGAGAGTATTGGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGT 1742

Qy       1681 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1743 ACAGTCATCGTCCCCTTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTT 1802

Qy       1741 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGT 1784
             |||||||||||||||||||||||||||||||||||||||||||||
Db       1803 GAAGACACATATGGGGAGTTGGAATTCAAGAATGATGAAACTGT 1846
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RESULT 11
US-10-114-153-5
; Sequence 5, Application US/10114153
; Publication No. US20030185815A1

; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251

; SEQ ID NO 5
; LENGTH: 2685
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2685)
US-10-114-153-5

Query Match 91.0%; Score 1694.8; DB 15; Length 2685;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1725; Conservative 0; Mismatches 27; Indels 4; Gaps 1;

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Qy         86 GAGCAGAGGCTGGTGGCTCAGGGGACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTT 145
               || | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 GATCCGAGGCTGGTGGCTCAGGGGACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTT 61

Qy        146 CAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTT 205
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CAGGGTCATCGGACTGCAAGGAGGGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTT 121

Qy        206 CCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCC 265
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CCCTTGGGGACAAGATTGCCAGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCC 181

Qy        266 TTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAG 325
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 TTGGGGTGTCCATCATTGCTGACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAG 241

Qy        326 AGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAACCACTATTCGGGTCT 385
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 AGAGGGAGGTGACAATTAAGAAACCCAATGGAGAAACCAGCACAACCACTATTCGGGTCT 301

Qy        386 GGAATGAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATAC 445
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GGAATGAAACTGTCTCCAACCTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATAC 361

Qy        446 TCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTA 505
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTCATTGCTGGTGATCTGGGACCTTCTA 421

Qy        506 CCATTGTAGGGAGTGCAGCCTTCAACATGTTCATCATCATTGGCATCTGTGTCTACGTGA 565
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 CCATTGTAGGGAGTGCAGCCTTCAACATGTTCATCATCATTGGCATCTGTGTCTACGTGA 481

Qy        566 TCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTTCATCACCGCTGCTT 625
               |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        482 TCCCAGACGGAGAGACTCGCAAGATCAAACATCTACGAGTCTTCTTCATCACCGCTGCTT 541

Qy        626 GGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGG 685
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 GGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTTCTCCCCTGGTGTGG 601

Qy        686 TCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCT 745
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 TCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTGTGTCCTTCTGGCCT 661
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Qy        746 GGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACA 805
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 GGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAAGTACCGCACAGACA 721

Qy        806 AACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATG 865
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 AACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGGCATTGAGATGGATG 781

Qy        866 GGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAAG 925
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 GGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCTGGAAGGGAAGGAAG 841

Qy        926 TGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAG 985
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 TGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAAGCAAAAACACCCAG 901

Qy        986 AGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAACAGA 1045
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        902 AGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAACAGA 961

Qy       1046 AGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCC 1105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        962 AGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAATATCC 1021

Qy       1106 TGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCG 1165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1022 TGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCACACCG 1081

Qy       1166 ATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGG 1225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 ATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAGTGCCTGG 1141

Qy       1226 AGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCA 1285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 AGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCAAAGACCA 1201

Qy       1286 TGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCA 1345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1202 TGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTATGAGTTCA 1261

Qy       1346 CAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAA 1405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1262 CAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTGGGCATAA 1321

Qy       1406 TTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCA 1465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1322 TTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAATGTCCGCA 1381

Qy       1466 TAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGC 1525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1382 TAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTTCCCTTGC 1441

Qy       1526 CTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATG 1585
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1442 CTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGATGACCATG 1501

Qy       1586 CAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGTGTTATGG 1645
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1502 CAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGTGTTATGG 1561

Qy       1646 AGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCCTTTAGGACAG 1705
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1562 AGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCCTTTAGGACAG 1621

Qy       1706 TAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAAT 1765
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1622 TAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAGTTGGAAT 1681

Qy       1766 TCAAGAATGATGAAACTGTATGTGACAGACAGGAAGCTGACTATGGAAGAAGAGGAGGCC 1825
                ||||||||||||||||    ||||| |  ||  | | | |  || | ||| |||||||
Db       1682 TCAAGAATGATGAAAC----TGTGAAAACCATAAGGGTTAAAATAGTAGATGAGGAGGAA 1737

Qy       1826 AAGAGGATAGCAGAGA 1841
                |    |    |||||
Db       1738 TACGAAAGGCAAGAGA 1753


RESULT 12
US-10-029-386-20265
; Sequence 20265, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR GENE
;  TITLE OF INVENTION:  EXPRESSION ANALYSIS TWO
;  FILE REFERENCE: AEOMICA-X-2
;  CURRENT APPLICATION NUMBER: US/10/029,386
;  CURRENT FILING DATE:  2001-12-20
;  NUMBER OF SEQ ID NOS: 34288
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 20265
;   LENGTH: 823
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AL160191.1
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
;   OTHER INFORMATION: SWISSPROT HIT: P57103, EVALUE 0.00e+00
;   OTHER INFORMATION: EST_HUMAN HIT: BI913344.1, EVALUE 0.00e+00
;   OTHER INFORMATION: NT HIT: gi15147253, EVALUE 0.00e+00
US-10-029-386-20265

  Query Match             44.1%;  Score 821.4;  DB 15;  Length 823;
  Best Local Similarity   99.9%;  Pred. No. 1.2e-255;
  Matches  822;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        432 TGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTCATTGCTGGTGA 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGCTCCTGAGATACTCCTCTCTTTAATTGAGGTGTGTGGTCATGGGTTCATTGCTGGTGA 60
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Qy        492 TCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATCATCATTGGCAT 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCTGGGACCTTCTACCATTGTAGGGAGTGCAGCCTTCAACATGTTCATCATCATTGGCAT 120

Qy        552 CTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTT 611
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGTGTCTACGTGATCCCAGACGGAGAGACTCGCAAGATCAAGCATCTACGAGTCTTCTT 180

Qy        612 CATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTT 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CATCACCGCTGCTTGGAGTATCTTTGCCTACATCTGGCTCTATATGATTCTGGCAGTCTT 240

Qy        672 CTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTG 731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTCCCCTGGTGTGGTCCAGGTTTGGGAAGGCCTCCTCACTCTCTTCTTCTTTCCAGTGTG 300

Qy        732 TGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAA 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTCCTTCTGGCCTGGGTGGCAGATAAACGACTGCTCTTCTACAAATACATGCACAAAAA 360

Qy        792 GTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGG 851
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTACCGCACAGACAAACACCGAGGAATTATCATAGAGACAGAGGGTGACCACCCTAAGGG 420

Qy        852 CATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCT 911
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CATTGAGATGGATGGGAAAATGATGAATTCCCATTTTCTAGATGGGAACCTGGTGCCCCT 480

Qy        912 GGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAA 971
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGAAGGGAAGGAAGTGGATGAGTCCCGCAGAGAGATGATCCGGATTCTCAAGGATCTGAA 540

Qy        972 GCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCT 1031
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAAAAACACCCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCT 600

Qy       1032 TTCCCACCAACAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGG 1091
              |||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db        601 TTCCCACCAACAGAAGAGCCGTGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGG 660

Qy       1092 TGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAG 1151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGCAGGCAATATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAG 720

Qy       1152 CGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTC 1211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CGAGGTGCACACCGATGAGCCTGAGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTC 780

Qy       1212 TTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTG 1254
              |||||||||||||||||||||||||||||||||||||||||||
Db        781 TTACCAGTGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTG 823
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RESULT 13
US-09-901-419-1
; Sequence 1, Application US/09901419

; Patent No. US20020069421A1
; GENERAL INFORMATION:
; APPLICANT: The Curators of the University of Missouri
; TITLE OF INVENTION: LARGE SCALE EXPRESSION AND PURIFICATION OF RECOMBINANT
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: UMO1531.1
; CURRENT APPLICATION NUMBER: US/09/901,419
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/218,125
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4087
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (268)..(3180)
; NAME/KEY: sig_peptide
; LOCATION: (268)..(363)
; NAME/KEY: misc_feature
; LOCATION: (3178)
; OTHER INFORMATION: A Poly (H) affinity tag comprising 6 His residues
; OTHER INFORMATION: have been inserted at the C-Terminus end of the
; OTHER INFORMATION: coding region of the protein
US-09-901-419-1

Query Match 43.5%; Score 810.6; DB 9; Length 4087;
Best Local Similarity 68.5%; Pred. No. 9.8e-252;
Matches 1211; Conservative 0; Mismatches 519; Indels 39; Gaps 5;

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Qy          46 TTTGGGCTGGTTACCTTTGTGCTCTTCCTGAATGGTCTTCGAGCAGAGGCTGGTGGCTCA 105
               |||    || |  || | |||    || ||  |   | |   |   |     |||
Db         307 TTTCACGTGATAGCCATGGTGGCTCTCTTGTTTTCCCATGTGGACCATATAAGTGCTGAG 366

Qy         106 GGGGACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAG 165
                 ||  ||  | |   |||  |  | | ||     ||| | || || |   |||| |||
Db         367 ACAGAAATGGAAGGAGAAGGCAACGAGACTGGCGAGTGTACTGGCTCCTATTACTGTAAG 426

Qy         166 GAGGGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCC 225
                |||| || ||  | || || ||| | ||  || |||||||| |||| ||||| |||||
Db         427 AAGGGGGTGATTTTACCCATTTGGGAGCCCCAGGACCCTTCCTTTGGAGACAAAATTGCT 486

Qy         226 AGGGTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCT 285
               || |  | ||| |||||.|.|||||| || | |||||||| ||||| || || |||||||||
Db         487 AGAGCGACTGTGTATTTTGTGGCCATGGTCTACATGTTTCTTGGAGTCTCAATCATTGCT 546

Qy         286 GACCGCTTCATGGCATCTATTGAAGTCATCACCTCTCAAGAGAGGGAGGTGACAATTAAG 345
               ||||| |||||| | ||||| |||||||||| |||||||||  ||  | || || |||
Db         547 GACCGGTTCATGTCCTCTATAGAAGTCATCACGTCTCAAGAGAAAGAAATCACCATAAAG 606

Qy         346 AAACCCAATGGAGAAACCAGCACAACCACTATTCGGGTCTGGAATGAAACTGTCTCCAAC 405
               |||||||||||||| |||| ||  || ||| |  || |||||||||| || || ||||||
Db         607 AAACCCAATGGAGAGACCACCAAGACAACTGTGAGGATCTGGAATGAGACAGTGTCCAAC 666

Qy         406 CTGACCCTTATGGCCCTGGGTTCCTCTGCTCCTGAGATACTCCTCTCTTTAATTGAGGTG 465
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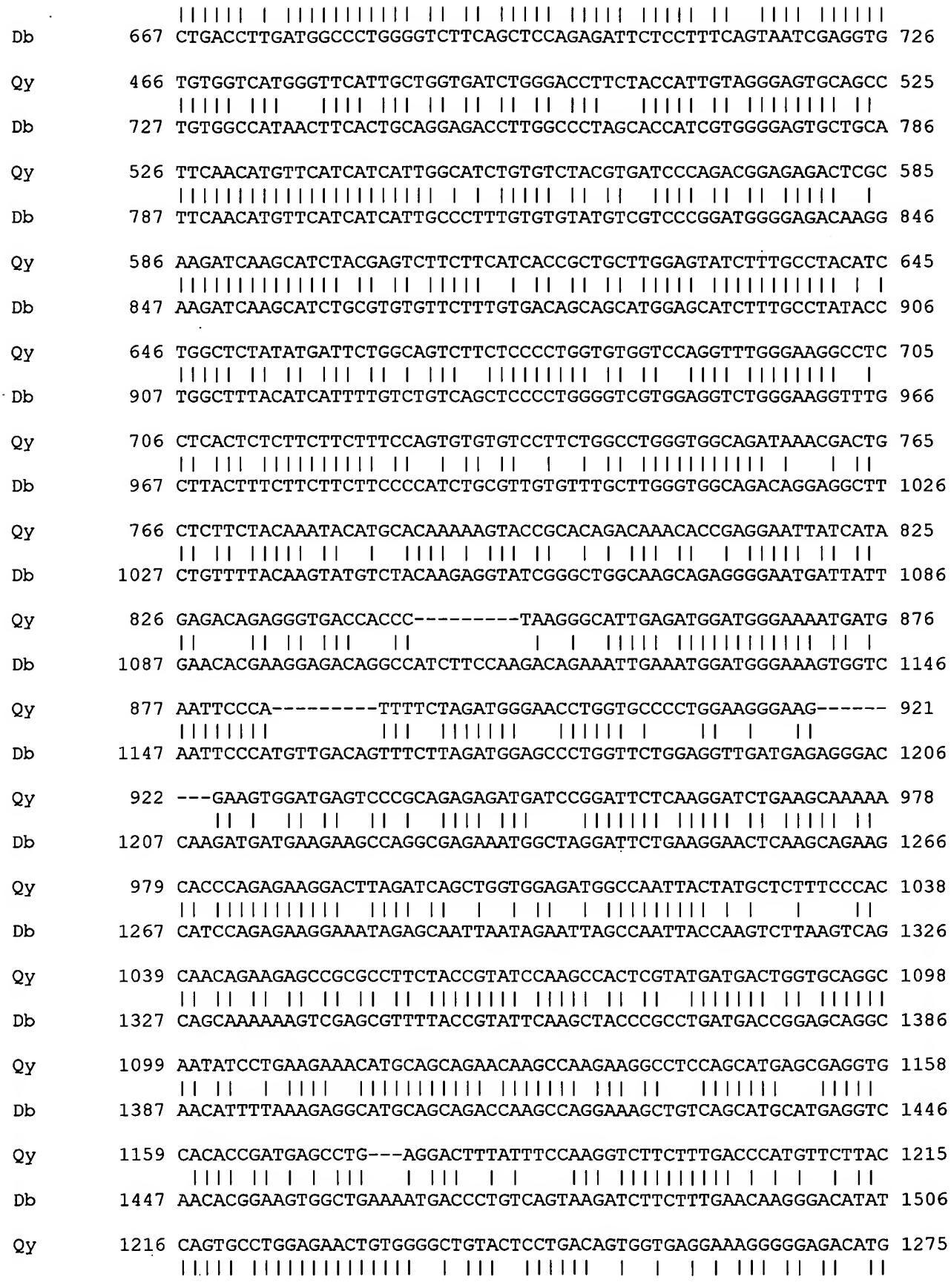

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Db       1507 CAGTGTCTGGAGAACTGTGGCACAGTAGCCCTGACCATTATCCGCAGAGGTGGTGATTTG 1566

Qy       1276 TCAAAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGAC 1335
              | || ||  ||| ||| |||| || ||||||||||||  | ||||||| ||  ||||
Db       1567 ACCAACACTGTGTTTGTTGACTTCAGAACAGAGGATGGCACAGCCAATGCTGGATCTGAT 1626

Qy       1336 TATGAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCC 1395
              || || || || || || || |||||  | |||||  || ||||||||||||||  ||
Db       1627 TACGAATTTACCGAAGGAACTGTGGTCTTTAAGCCTGGTGAGACCCAGAAGGAAATCAGA 1686

Qy       1396 GTGGGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGC 1455
              || ||||| |||||||| ||||| |||||||||||||  | ||| ||||      | |||
Db       1687 GTTGGCATCATTGATGATGACATCTTTGAGGAGGATGAGAATTTCCTTGTGCATCTCAGC 1746

Qy       1456 AATGTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGT 1515
              || |||    ||     |||     | || || || || |    |||          ||||
Db       1747 AACGTCAAAGTATCTTTGGAAGCCTCGGAAGACGGCATCCTGGAAGC---------CAGT 1797

Qy       1516 CTTCCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGAT 1575
              | |  ||   | |  |||  ||| |  ||||| |     ||||| || || || || |||
Db       1798 CATGTCTCTACCCTTGCTTGCCTGGGATCCCCCTCCACTGCCACCGTGACTATTTTTGAT 1857

Qy       1576 GATGACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATT 1635
              |||||||||| |||||||| ||||||||          | |||||| |||||||| |||
Db       1858 GATGACCATGCTGGCATCTTTACTTTTGAGGAACCGGTGACTCATGTGAGTGAGAGCATT 1917

Qy       1636 GGTGTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCC 1695
              ||  | |||||||| || |||||| | ||||| || || || || |  || ||||| |||
Db       1918 GGCATCATGGAGGTGAAAGTTCTGAGAACATCTGGAGCACGTGGAAATGTTATCGTTCCC 1977

Qy       1696 TTTAGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGG 1755
              | || |||  | || ||||| ||||  ||||| || |||||||||| |||||||  ||
Db       1978 TATAAGACCATTGAGGGGACCGCCAGAGGTGGAGGGGAGGACTTTGAGGACACATGCGGA 2037

Qy       1756 GAGTTGGAATTCAAGAATGATGAAACTGT 1784
              ||| | || ||| ||||||| |||| |||
Db       2038 GAGCTCGAGTTCCAGAATGACGAAATTGT 2066


RESULT 14
US-09-864-761-16939
; Sequence 16939, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;  APPLICANT: Penn, Sharron G.
;  APPLICANT:  Rank, David R.
;  APPLICANT:  Hanzel, David K.
;  APPLICANT:  Chen, Wensheng
;  TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR
;  TITLE OF INVENTION:  GENE EXPRESSION ANALYSIS BY MICROARRAY
;  FILE REFERENCE: Aeomica-X-1
;  CURRENT APPLICATION NUMBER: US/09/864,761
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: US 60/180,312
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: US 60/207,456
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;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: US 09/632,366
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00662
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00661
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00670
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: US 60/234,687
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: US 09/608,408
;  PRIOR FILING DATE: 2000-06-30
;  PRIOR APPLICATION NUMBER: US 09/774,203
;  PRIOR FILING DATE: 2001-01-29
;  NUMBER OF SEQ ID NOS: 49117
;  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 16939
;   LENGTH: 1836
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: MAP TO AC007281.3
;   OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.64
;   OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.68
;   OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.69
;   OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.1
;   OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.83
;   OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
;   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.68
;   OTHER INFORMATION: NT HIT: X91213.1, EVALUE 0.00e+00
;   OTHER INFORMATION: EST_HUMAN HIT: AW452398.1, EVALUE 0.00e+00
;   OTHER INFORMATION: SWISSPROT HIT: P32418, EVALUE 0.00e+00
US-09-864-761-16939

  Query Match             42.1%;  Score 785.2;  DB 9;  Length 1836;
  Best Local Similarity   68.3%;  Pred. No. 1.1e-243;
  Matches 1166;  Conservative    0;  Mismatches  503;  Indels   39;  Gaps    4;
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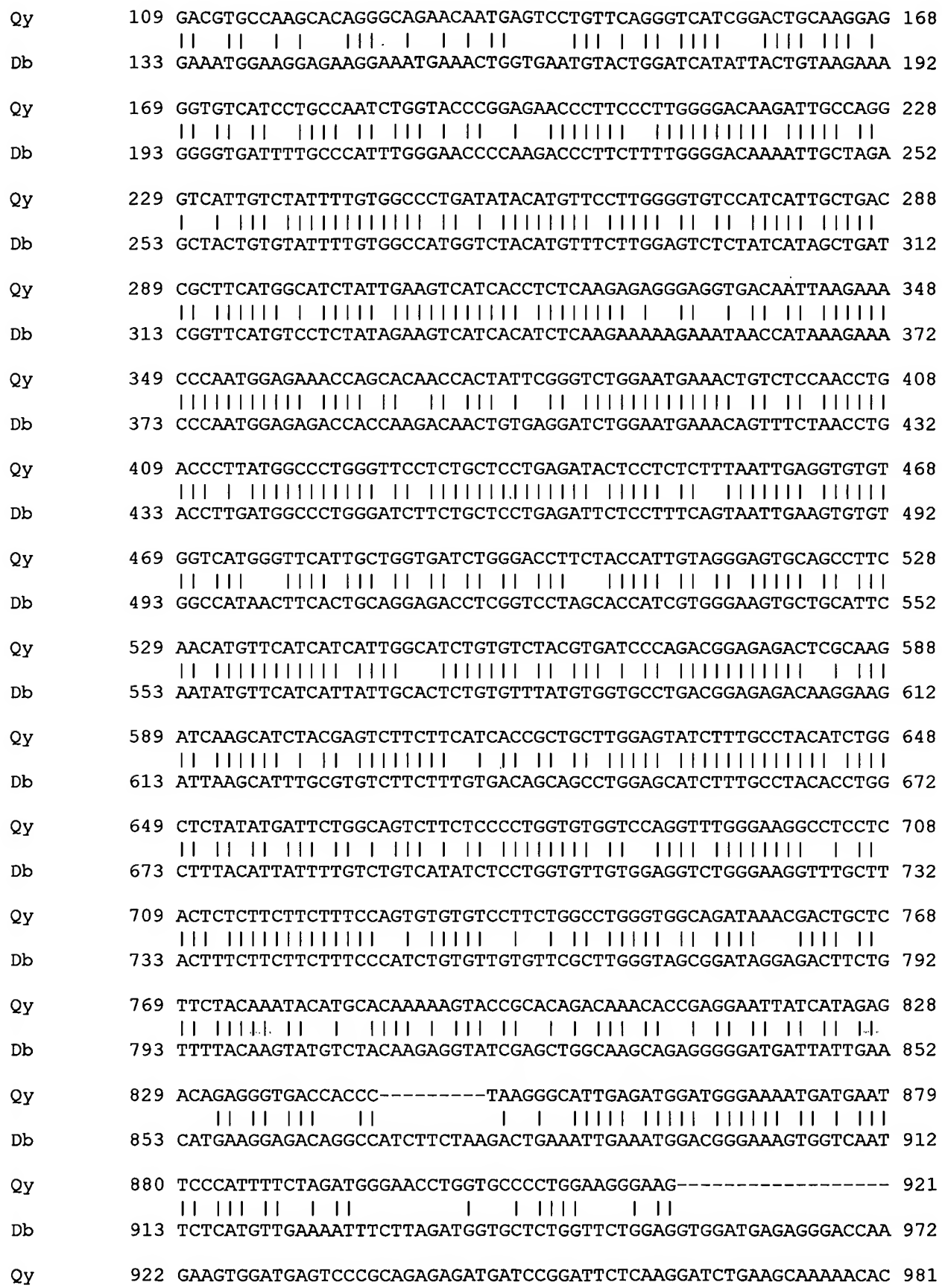

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Qy        982 CCAGAGAAGGACTTAGATCAGCTGGTGGAGATGGCCAATTACTATGCTCTTTCCCACCAA 1041

Db       1033 CCAGATAAAGAAATAGAGCAATTAATAGAATTAGCTAACTACCAAGTCCTAAGTCAGCAG 1092

Qy       1042 CAGAAGAGCCGCGCCTTCTACCGTATCCAAGCCACTCGTATGATGACTGGTGCAGGCAAT 1101

Db       1093 CAAAAAAGTAGAGCATTTTATCGCATTCAAGCTACTCGCCTCATGACTGGAGCTGGCAAC 1152

Qy       1102 ATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCAC 1161

Db       1153 ATTTTAAAGAGGCATGCAGCTGACCAAGCAAGGAAGGCTGTCAGCATGCACGAGGTCAAC 1212

Qy       1162 ACCGATGAGCCTG---AGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAG 1218

Db       1213 ACTGAAGTGACTGAAAATGACCCTGTTAGTAAGATCTTCTTTGAACAAGGGACATATCAG 1272

Qy       1219 TGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCA 1278

Db       1273 TGTCTGGAGAACTGTGGTACTGTGGCCCTTACCATTATCCGCAGAGGTGGTGATTTGACT 1332

Qy       1279 AAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTAT 1338

Db       1333 AACACTGTGTTTGTTGACTTCAGAACAGAGGATGGCACAGCAAATGCTGGGTCTGATTAT 1392

Qy       1339 GAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTG 1398

Db       1393 GAATTTACTGAAGGAACTGTGGTGTTTAAGCCTGGTGATACCCAGAAGGAAATCAGAGTG 1452

Qy       1399 GGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAAT 1458

Db       1453 GGTATCATAGATGATGATATCTTTGAGGAGGATGAAAATTTCCTTGTGCATCTCAGCAAT 1512

Qy       1459 GTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTT 1518

Db       1513 GTCAAAGTATCTTCTGAAGCTTCAGAAGATGGCATACTGGAAGC---------CAATCAT 1563

Qy       1519 CCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGAT 1578

Db       1564 GTTTCTACACTTGCTTGCCTCGGATCTCCCTCCACTGCCACTGTAACTATTTTTGATGAT 1623

Qy       1579 GACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGT 1638

Db       1624 GACCACGCAGGCATTTTTACTTTTGAGGAACCTGTGACTCATGTGAGTGAGAGCATTGGC 1683

Qy       1639 GTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCCTTT 1698

Db       1684 ATCATGGAGGTGAAAGTATTGAGAACATCTGGAGCTCGAGGAAATGTTATCGTTCCATAT 1743

Qy       1699 AGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAG 1758

Db       1744 AAAACCATCGAAGGGACTGCCAGAGGTGGAGGGGAGGATTTTGAGGACACTTGTGGAGAG 1803

Qy       1759 TTGGAATTCAAGAATGATGAAACTGTAT 1786
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Db       1804 CTCGAATTCCAGAATGATGAAATTGTGT 1831


RESULT 15
US-10-357-930-24294
; Sequence 24294, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
;  APPLICANT: Schlegel. Robert
;  APPLICANT:  Endege, Wilson
;  APPLICANT:  Monahan, John
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
;  TITLE OF INVENTION:  HUMAN PROSTATE CANCER
;  FILE REFERENCE: MRI-007BCN
;  CURRENT APPLICATION NUMBER: US/10/357,930
;  CURRENT FILING DATE:  2003-02-04
;  PRIOR APPLICATION NUMBER: 09/785,276
;  PRIOR FILING DATE: 2003-02-16
;  PRIOR APPLICATION NUMBER: 60/183,319
;  PRIOR FILING DATE: 2000-02-17
;  PRIOR APPLICATION NUMBER: 60/189,862
;  PRIOR FILING DATE: 2000-03-16
;  PRIOR APPLICATION NUMBER: 60/207,454
;  PRIOR FILING DATE: 2000-05-25
;  PRIOR APPLICATION NUMBER: 60/211,314
;  PRIOR FILING DATE: 2000-06-09
;  PRIOR APPLICATION NUMBER: 60/219,007
;  PRIOR FILING DATE: 2000-07-18
;  PRIOR APPLICATION NUMBER: 60/255,281
;  PRIOR FILING DATE: 2000-12-13
;  NUMBER OF SEQ ID NOS: 62232
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 24294
;   LENGTH: 5438
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1, 2, 3, 4, 5437, 5438
;   OTHER INFORMATION: n = A,T,C or G
US-10-357-930-24294

  Query Match             42.1%;  Score 784.8;  DB 18;  Length 5438;
  Best Local Similarity   68.3%;  Pred. No. 2.9e-243;
  Matches 1165;  Conservative    0;  Mismatches  502;  Indels   39;  Gaps    4;

Qy        109 GACGTGCCAAGCACAGGGCAGAACAATGAGTCCTGTTCAGGGTCATCGGACTGCAAGGAG 168
              ||  ||  | |   |||  |  | | ||     ||| | || ||||   |||| ||| |
Db        245 GAAATGGAAGGAGAAGGAAATGAAACTGGTGAATGTACTGGATCATATTACTGTAAGAAA 304

Qy        169 GGTGTCATCCTGCCAATCTGGTACCCGGAGAACCCTTCCCTTGGGGACAAGATTGCCAGG 228
              || ||  ||  |||| || ||| | ||  |  |||||||  |||||||||| ||||| ||
Db        305 GGGGTGATTTTGCCCATTTGGGAACCCCAAGACCCTTCTTTTGGGGACAAAATTGCTAGA 364

Qy        229 GTCATTGTCTATTTTGTGGCCCTGATATACATGTTCCTTGGGGTGTCCATCATTGCTGAC 288
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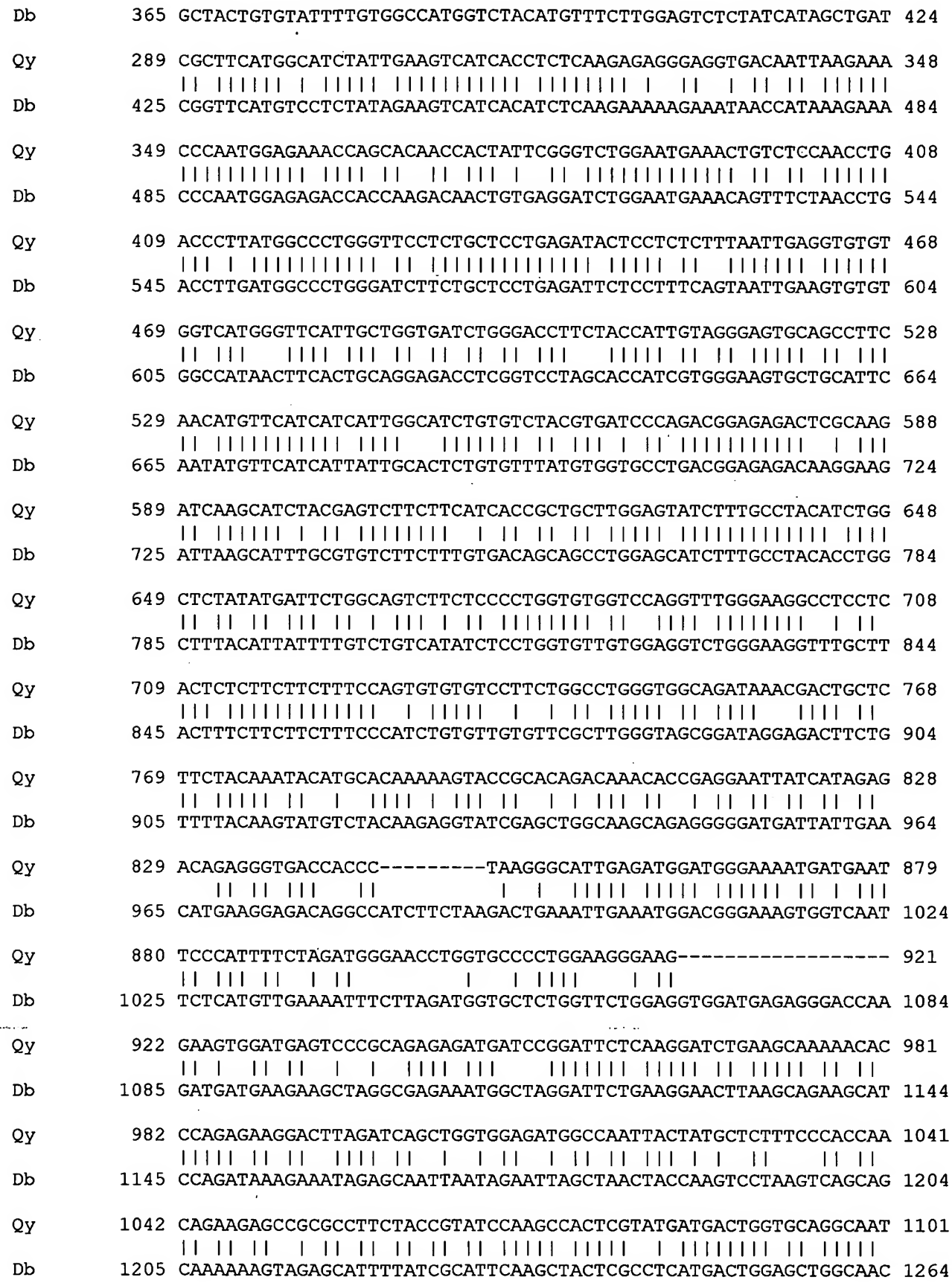

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Qy       1102 ATCCTGAAGAAACATGCAGCAGAACAAGCCAAGAAGGCCTCCAGCATGAGCGAGGTGCAC 1161
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Db       1265 ATTTTAAAGAGGCATGCAGCTGACCAAGCAAGGAAGGCTGTCAGCATGCACGAGGTCAAC 1324

Qy       1162 ACCGATGAGCCTG---AGGACTTTATTTCCAAGGTCTTCTTTGACCCATGTTCTTACCAG 1218
              || || | | |||   | |||  | ||   ||| |||||||||| | | |  | || |||
Db       1325 ACTGAAGTGACTGAAAATGACCCTGTTAGTAAGATCTTCTTTGAACAAGGGACATATCAG 1384

Qy       1219 TGCCTGGAGAACTGTGGGGCTGTACTCCTGACAGTGGTGAGGAAAGGGGGAGACATGTCA 1278
              || ||||||||||||||  ||||   ||| ||  |  |  | | ||| || ||  || |
Db       1385 TGTCTGGAGAACTGTGGTACTGTGGCCCTTACCATTATCCGCAGAGGTGGTGATTTGACT 1444

Qy       1279 AAGACCATGTATGTGGACTACAAAACAGAGGATGGTTCTGCCAATGCAGGGGCTGACTAT 1338
              || ||  ||| ||| |||| || ||||||||||||  | || ||||| ||| |||| |||
Db       1445 AACACTGTGTTTGTTGACTTCAGAACAGAGGATGGCACAGCAAATGCTGGGTCTGATTAT 1504

Qy       1339 GAGTTCACAGAGGGCACGGTGGTTCTGAAGCCAGGAGAGACCCAGAAGGAGTTCTCCGTG 1398
              || || || || || || |||||  | ||||| || || ||||||||||  ||   |||
Db       1505 GAATTTACTGAAGGAACTGTGGTGTTTAAGCCTGGTGATACCCAGAAGGAAATCAGAGTG 1564

Qy       1399 GGCATAATTGATGACGACATTTTTGAGGAGGATGAACACTTCTTTGTAAGGTTGAGCAAT 1458
              || || || ||||| || || |||||||||||||| | ||| ||||     | ||||||
Db       1565 GGTATCATAGATGATGATATCTTTGAGGAGGATGAAAATTTCCTTGTGCATCTCAGCAAT 1624

Qy       1459 GTCCGCATAGAGGAGGAGCAGCCAGAGGAGGGGATGCCTCCAGCAATATTCAACAGTCTT 1518
              |||    ||      ||     |||| || || || |    |||          || || |
Db       1625 GTCAAAGTATCTTCTGAAGCTTCAGAAGATGGCATACTGGAAGC---------CAATCAT 1675

Qy       1519 CCCTTGCCTCGGGCTGTCCTAGCCTCCCCTTGTGTGGCCACAGTTACCATCTTGGATGAT 1578
                 |   | |  |||  ||| |  || || |     ||||| || || || || ||||||
Db       1676 GTTTCTACACTTGCTTGCCTCGGATCTCCCTCCACTGCCACTGTAACTATTTTTGATGAT 1735

Qy       1579 GACCATGCAGGCATCTTCACTTTTGAATGTGATACTATTCATGTCAGTGAGAGTATTGGT 1638
              ||||| |||||||| || ||||||||      |   | |||||| |||||||| |||||
Db       1736 GACCACGCAGGCATTTTTACTTTTGAGGAACCTGTGACTCATGTGAGTGAGAGCATTGGC 1795

Qy       1639 GTTATGGAGGTCAAGGTTCTGCGGACATCAGGTGCCCGGGGTACAGTCATCGTCCCCTTT 1698
               | |||||||| || ||  || | ||||| || || || || |  || ||||| || | |
Db       1796 ATCATGGAGGTGAAAGTATTGAGAACATCTGGAGCTCGAGGAAATGTTATCGTTCCATAT 1855

Qy       1699 AGGACAGTAGAAGGGACAGCCAAGGGTGGCGGTGAGGACTTTGAAGACACATATGGGGAG 1758
              |  ||  | |||||||| ||||  ||||| || ||||| ||||| ||||| | ||| |||
Db       1856 AAAACCATCGAAGGGACTGCCAGAGGTGGAGGGGAGGATTTTGAGGACACTTGTGGAGAG 1915

Qy       1759 TTGGAATTCAAGAATGATGAAACTGT 1784
               | |||||| |||||||||||| |||
Db       1916 CTCGAATTCCAGAATGATGAAATTGT 1941
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Search completed: January 22, 2005, 18:16:37
Job time : 992.631 secs